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Volume 15

2026-04-28

ERRATA CORRIGE

- *Coprinellus aureodissemminatus from Australia, C. punjabensis from Dominican Republic and notes on C. disseminatisimilis. Errata Corrige*

Voto, P; Bougher, NL; Angelini, C. **MycolObs** 15: 1–1

ARTICLES / ARTICOLI

- *First record of *Podaxis pistillaris* (Basidiomycetes, Agaricaceae) in the Dominican Republic*
Angelini, C; Voto, P. **MycolObs** 15: 2–6
- *From cryptic gene clusters to bioactive metabolites: the role of AI in advancing fungal endophytes research*
Lakshmanan, M; Meenambiga, SS; Kaliyaperumal, KA; Rajagopal, K. **MycolObs** 15: 7–24
- *Spore dextrinoidity in the genus *Cortinarius* s.l. / Destrinoidia sporale nel genere *Cortinarius* s.l.*
Raumi, M. **MycolObs** 15: 25–88
- *Novelties in Family *Psathyrellaceae*. Part IX*
Voto, P. **MycolObs** 15: 89–89

Mycological records from the regions / Rubrica di micologia dai territori

- **Hysteropeltella moravica* (Ascomycota, Dothideales) in Bosnia*
Trivič, D. **MycolObs** 15: 90-92

Gruppo Micologico e Naturalistico DLF Verona

Via XX Settembre 17, I-37193 Verona, Italia

<https://www.micologiadlfvr.it>

info@veronamicologica.it

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Mycena meliigena (Berk. & Cooke) Sacc.

ERRATA CORRIGE

***Coprinellus aureodisseminatus* from Australia, *C. punjabensis* from Dominican Republic and notes on *C. disseminatisimilis*. Errata Corrige**

Pietro Voto, Neale L. Bougher & Claudio Angelini

MycolObs 13:1–17 (4 August 2025)

The article incorrectly reported the microcharacters of the Dominican collection of *Coprinopsis punjabensis*. They are correctly reported below.

Basidiospores [35, 1, 1] (6.9)7.2–8.8(9.5) × (4.2)4.4–5.2(5.5) µm, mean 8.0 × 4.8 µm, Q = 1.57–1.76(1.83), Q mean = 1.67; in face view ovoid to narrowly submitriform, base obtuse to rounded in shorter spores or tapering in longer spores; in side view adaxially flattened to subamygdaliform; in water brown with a reddish shade, smooth-walled; germ pore 1.1–1.4 µm, distinct, central, truncate.

Basidia 19.0–30.0 × 7.0–11.0 µm, clavate to narrowly clavate, 4-spored.

Pleurocystidia and *Cheilocystidia* absent.

Pileipellis an epithelium composed of 13.0–40.0 µm broad elements.

Pileocystidia 69.8–123.8 × 12.5–20.6 µm, apex 7.0–12.4 µm broad, long-necked utriform to almost cylindraceous, neck often slightly restricted before the apical part; thin-walled, hyaline; scattered.

Caulocystidia 51.6–106.9 × 7.4–20.2 µm, apex 5.6–17.6 µm broad, long-neck utriform to cylindric, neck sometimes slightly restricted before the apical part; thin-walled, hyaline; mostly found in the lower half of the stipe.

Clamp connections not found.

The original article can be found at <https://www.mycolobs-journal.org/Volumi/MycolObs13p01-17.pdf>

Citation of the original article: Voto, P; Bougher, NL; Angelini, C (2025) *Coprinellus aureodisseminatus* from Australia, *C. punjabensis* from Dominican Republic and notes on *C. disseminatisimilis*. *MycolObs* 13:1–17

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First record of *Podaxis pistillaris* (Basidiomycetes, Agaricaceae) in the Dominican Republic

Claudio Angelini^{1,2,a}, Pietro Voto^{3,b}

¹Jardín Botánico Nacional Dr. Rafael Ma. Moscoso, Santo Domingo, Dominican Republic

²Via Cappuccini 78/8, I-33170 Pordenone, Italy

³Via Garibaldi 173, I-45010 Villadose (RO), Italy

^aclaudio_angelini@libero.it; <https://orcid.org/0000-0002-5485-6889>

^bpietrovoto@libero.it; <https://orcid.org/0000-0003-1922-1324>

*Corresponding author: claudio_angelini@libero.it

Key words:

Agaricomycetes

Agaricales

taxonomy

Abstract: *Podaxis pistillaris*, a species widely distributed in desert and semi-desert habitats worldwide, is reported for the first time from the Dominican Republic. Although the spore size is slightly smaller than the expected range, all other characteristics, including the sand-dwelling habitat, are consistent with this taxon. An ITS sequence also supports this identification.

INTRODUCTION

Based on unconfirmed reports of the presence of "desert mushrooms" in the Dominican Republic, one of us, C. A., after extensively searching for fungal species belonging to the genus *Podaxis* Dev. in various arid, sandy or semi-desert areas, finally found it fruiting in abundance in a sandy area close to the north-western Dominican ocean coast, adjacent to the Estero Hondo Marine Mammal Sanctuary in the province of Porto Plata. Initially, this species of *Podaxis* was thought to be specific to the Neotropics; however, subsequent morphological and molecular studies revealed that it belongs to the most widely distributed species worldwide, *Podaxis pistillaris* (L.) Fr. This was also confirmed by a recent and comprehensive study on the genus *Podaxis* conducted by Li *et al.* (2023), which, on a phylogenetic basis, demonstrated the presence of this species in the Caribbean (Jamaica) and Central America (Mexico).

MATERIALS AND METHODS

Fresh basidiomata of the Dominican collection were photographed in situ by C. A. using a Nikon Coolpix 8400 camera and immediately dried thereafter. Macroscopic characters were observed from the photographs. Microscopy was performed by P. V. Micrographs of the spores were made from dried material suspended in water using a Nikon Coolpix A10 camera and a binocular Leica microscope DME.

TAXONOMY

Podaxis pistillaris (L.) Fr. (as '*Podaxon pistillaris*')
Syst. Mycol. (Lundae) 3(1): 63 (1829)

Syst. Mycol. (Lundae) 3(1): 63 (1829)

Synonyms: see Li *et al.* (2023)

Macroscopic characters

Basidiocarp secotioid, stipitate, 100–250 mm tall, dry, indehiscent at maturity.

Pileus 40–95 mm in height × 25–45 mm diam at maturity, narrowly ellipsoid to paraboloid, white to pale cream, dry; surface shiny, consisting of an initially persistent membranaceous peridium; peridium margin initially adherent to the stem and breaking at maturity into fibrous scales to release spores.

Lamellae absent, basidiospore-producing tissue filamentous-powdery, initially white in colour, then yellowish-olive green, yellowish ochre-brown to dark brown to almost black.

Stipe 100–220 × 10–15 mm at maturity below the pileus, cylindrical with a bulbous base; dry, hard and woody, spiral, fibrous, striate or broken into fibrous scales; white to yellowish brown staining bright red. *Annulus* and *volva* absent.



Podaxis pistillaris in habitat. ANGE1866

C. Angelini

*Podaxis pistillaris* in habitat. ANGE1866

C. Angelini

Microscopic characters

Spores (8.3)9.0–10.6(12.8) × (7.7)8.3–9.5(11.3) μm, Q = 1.01–1.14, those well pigmented mostly regularly subglobose to globose or sometimes obovoid, those immature-hyaline varying to ellipsoid or deformed; thick-walled and with another distinct inner wall 6–9 μm inside; the most pigmented darkish brownish-orangish in water; spore print light yellowish-olivaceous; germ pore swollen and with a distinct medulla up to the inner wall; without apiculus.

Collections examined and Habitat: Dominican Republic, province of Puerto Plata, municipal district of Estero Hondo, in the protected area of the Estero Hondo Marine Mammal Sanctuary, gregarious in an arid-sandy area close to the ocean coast, 24 March 2023, C. Angelini ANGE1866 (JBSD141869), GenBank acc. no. UDB07674839.

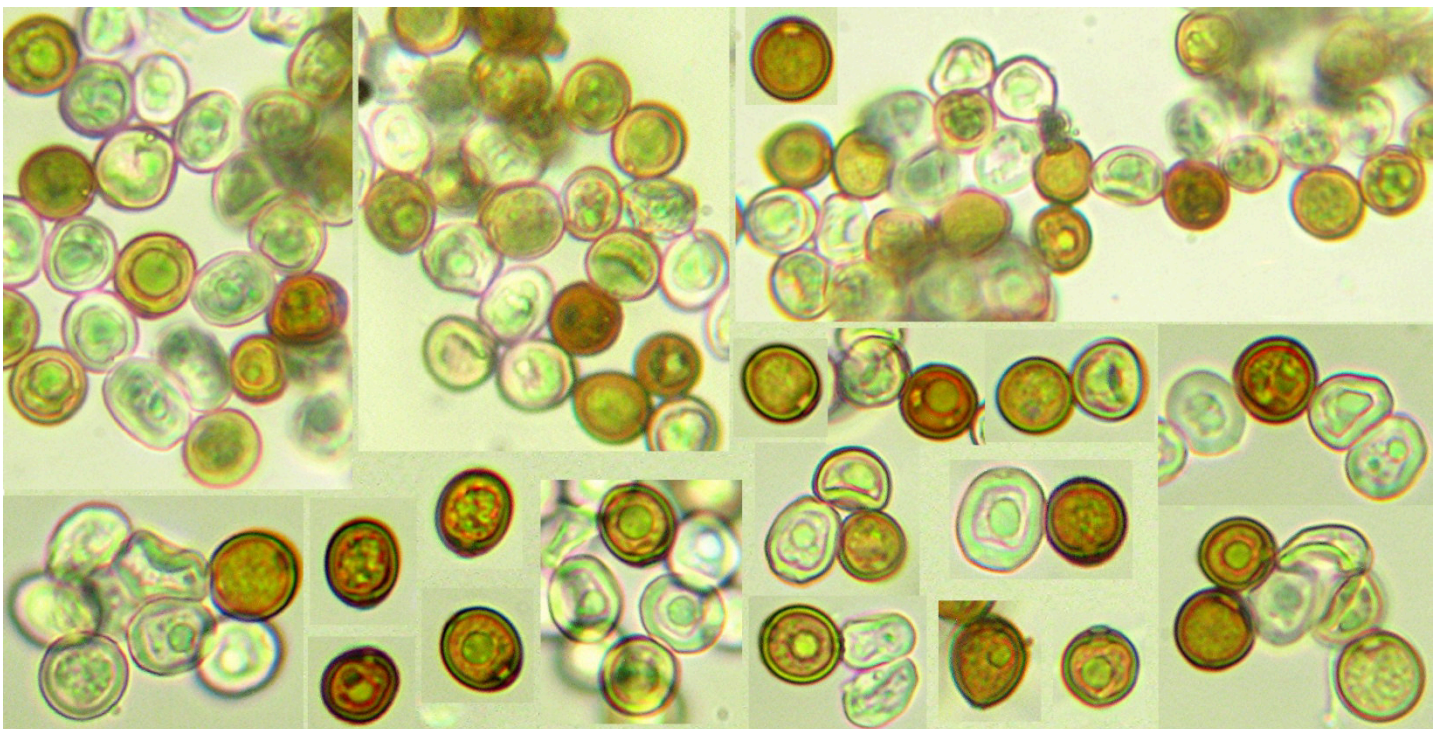
NOTES

The spore range of our collection was carefully studied to determine whether it was morphologically comparable with taxa of *Podaxis* sect. *Parvispora* McKnight (McKnight 1985), especially with *P. argentinus* Speg. and *P. longii* McKnight reported from Central and Southern America. To date, neither of these two species has any molecular data and consequently no phylogenetic comparison could be made. However, *P. argentinus* has distinctly smaller spores with an indistinct germ pore; while *P. longii*, though having somewhat comparable but averagely smaller spores [(5.5)6–10(13) × (4.4)5–8 μm] with a smaller germ pore (0.9–1.1 μm broad), differs in distinctly larger basidiomes (150–450 mm long with 15–40 mm broad stipes) and an equal to tapering, not swollen stipe base (McKnight 1985).



Podaxis pistillaris, section of the basidiomes. ANGE1866

C. Angelini



Podaxis pistillaris, spores in water. ANGE1866

P. Voto

Li *et al.* (2023) report the spores of *P. pistillaris* as (6.9)9.8–12.0(19.9) × (6.1)9.0–10.4 (18.5) µm (*Podaxis* sect. *Podaxis*). Our measurements are placed right at the lower level of this range probably because the specimens studied were not fully mature. The ITS sequence obtained from our collection places it fully in the large ‘clade 1’ that Li *et al.* (2023) recognise as representing *P. pistillaris* and which contains vouchers from Central and South America (Brazil, Ecuador, Jamaica, Mexico and Venezuela).

REFERENCES

- Li, GS; Leal-Dutra, CA; Cuesta-Maté, A; Conlon, BH; Peereboom, N; Beemelmans, C; Aanen, DK; Rosendahl, S; de Beer, ZW; Poulsen, M (2023) Resolution of eleven reported and five novel *Podaxis* species ,based on ITS phylogeny, phylogenomics, morphology, ecology, and geographic distribution. *Persoonia* **51**:257–279
<https://doi.org/10.3767/persoonia.2023.51.07>
- McKnight, KH (1985) The small-spored species of *Podaxis*. *Mycologia* **77**(1):24–35

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From cryptic gene clusters to bioactive metabolites: the role of AI in advancing fungal endophytes research

Manigundu Lakshmanan¹, Setti Sudharsan Meenambiga², Alagapuram Kaliyaperumal Kathiresan³, Kalyanaraman Rajagopal^{1*}

¹Department of Botany, Ramakrishna Mission Vivekananda College, Mylapore, Chennai – 600 004, India. (Affiliated to the University of Madras), Chennai-600004, Tamil Nadu, India

²Department of Bioengineering, School of Engineering, Vels Institute of Science, Technology and Advanced Studies (VISTAS), Chennai- 600117, Tamil Nadu, India

³Department of Microbiology, School of Life Sciences, Vels Institute of Science, Technology and Advanced Studies (VISTAS), Chennai- 600117, Tamil Nadu, India

*Corresponding author: krajagopal@rkmvc.ac.in

Key words:

artificial intelligence (AI)
BGCs
biosynthetic gene clusters
deep learning
drug discovery
machine learning
secondary metabolites

Abstract: This study reports on the current state of the application of AI in the study of Fungal Endophytes. It highlights how AI-powered processes help in the genome mining and BGC annotation; how they are used in predicting metabolite structure and biological activity; how AI-driven culture models can optimize fungal fermentation and expression; and how, in combination with multi-omics measurements, AI is a powerful instrument to unlock the metabolic potential of fungal endophytes. Finally, further fields of application of AI models in understanding secondary metabolisms and researching anticancer drugs are reported. A flowchart and multiple panels help illustrate and represent the topics treated.

INTRODUCTION

Plant endophytic microbiomes, particularly fungal endophytes, are increasingly recognized as a prolific, yet underexplored, source of bioactive secondary metabolites (SMs) with significant pharmaceutical potential (Rajagopal *et al.* 2012). Endophytic fungi isolated from hydrophytes demonstrated rich mycodiversity and significant biotechnological potential (Rajagopal *et al.* 2012). Particularly fungal endophytes of these microbial communities have demonstrated the capacity to produce compounds with anticancer, antiviral, and antibacterial activity, including well-known molecules like paclitaxel and cryptocyanin (Hashem *et al.* 2023; Adeleke & Babalola 2021). Antibiofilm activity and molecular docking studies of bioactive secondary metabolites have been carried from *Aspergillus nidulans* on oral *Candida albicans* (Meenambiga & Rajagopal 2018). Endophytic fungi derived from marine algae are also being studied (Kalyanaraman *et al.* 2025). The co-evolution of endophytes with their host plants has resulted in unique biosynthetic gene clusters (BGCs) that rival or exceed those found in free-living microbes (Pillay *et al.* 2022; Ali *et al.* 2024). However, many of these BGCs remain silent under standard laboratory conditions and this silence presents a major challenge for drug discovery in endophytes (Reen *et al.* 2015; Tomm, Ucciferri & Ross 2019). Recent emergence of multi-omics technology, including transcriptomics, metabolomics, regulomes, and genomics, has now provided the opportunity to rationally determine and map these dark biosynthesis-related pathways (Sagita *et al.* 2021; Bhardwaj *et al.* 2023; Chen *et al.* 2023; Hannigan *et al.* 2019; Riedling, Walker & Rokas 2024). In addition to making predictions on the best conditions to use in cultures or environmental stimuli to induce dormant groups of genes and understanding complex regulatory interactions, AI models can also be used to predict the most favourable conditions in supporting the growth of organisms as in BGC mining (Verma *et al.* 2023; Chowdhary, Arora & Sharma 2022, Shu *et al.* 2024). Simulating ecological dynamics of interactions among microbes and plants is also becoming popular in AI, with biocontrol to sustainable agriculture being some of the applications. It is a paradigm shift in the discovery of natural products through endophytes motivated by integration methods that involve natural intelligence, synthetic biology, systems biology, and bioinformatics (Gakuubi *et al.* 2021). This accruing progress of using plant endophytes as a new approach to natural drug discovery makes this

approach exceptionally promising. To fully deliver on this promise, it will be necessary to explore and exploit microbial metabolic dark matter in an organized manner with the help of a mix of genomics, AI, and functional validation methods (Sagita *et al.* 2021).

AI-POWERED GENOME MINING AND BGC ANNOTATION

One important recent development in artificial intelligence (AI) is deep learning (DL) as it has transformed genome mining in fungal endophytes by allowing more specific detection and annotation of biosynthetic gene clusters (BGCs). Widely applicable tools like DeepBGC that rely on convolutional neural networks (CNNs) trained on datasets of BGCs can allow more precise identification of the borders between BGCs even in complex fungal genomes where traditional metabolic markers are usually missing or altered (Hannigan *et al.* 2019; Roy *et al.* 2025; Zhou *et al.* 2025; Mansourvar *et al.* 2025) (Fig. 1 & 2, Table 1). Effector-GAN can predict fungal effector proteins using the generative adversarial networks and pretrained deep representation learning methods, particularly of fungal endophytes that often contain cryptic or unique clusters of genes due to the evolutionary changes in adaptation to various ecological niches and co-evolution with host plants (Gakuubi *et al.* 2021; Wang *et al.* 2022; Chen *et al.* 2023) (Fig. 1 & 2, Table 1). Endophyte research commonly uses draft genomes or metagenomic datasets due to microbial complexity and sequencing difficulties; these models enhance the detection of fragmented or novel BGCs (Theobald *et al.* 2018; Wang *et al.* 2025). In contrast to traditional metabolic markers that are often missing or altered, these AI-driven approaches provide a more robust framework for identifying BGCs. While conventional methods struggle with the complexity of draft genomes and fragmented datasets, AI models offer higher sensitivity and precision, enabling the discovery of cryptic biosynthetic gene clusters that were previously undetectable. AI-powered models help identify promoter elements, transcription factor binding sites, and epigenetic markers that control low-expression or silence clusters (Gupta *et al.* 2020; Liu *et al.* 2025). With the use of scoring systems based on structural novelty, predicted pharmacological potential, and biosynthetic feasibility, network-based prioritization frameworks have advanced beyond simple detection to incorporate outputs from genome mining tools such as antiSMASH, MIBiG, and PRISM (Ming *et al.* 2023; Yuan *et al.* 2023; Liu *et al.* 2022; Zakariyah *et al.* 2024; Kumari *et al.* 2025) (Fig. 1 & 2, Table 1). Bayesian inference models and graph neural networks (GNNs) are being utilized more and more to simulate metabolite pathway interactions and infer gene co-expression patterns, and endophytic fungal ITS data phylogenetic analysis are being obtained utilizing massive parallel Bayesian tree inference with exabytes (Montero-Vargas, Umaña-Jiménez, Escudero-Leiva & Chaverri-Echandi 2020; Pöttker *et al.* 2023) (Fig. 1 & 2, Table 1). This provides functional context and prioritizes BGCs that are most likely to produce bioactive compounds (Al Shami & Mousa 2026). The identification of desired clusters for subsequent uses, such as chemical profiling, synthetic biology, or heterologous expression, is further improved by combining AI algorithms with multi-omics data (e.g. transcriptomics, epigenomics, and metabolomics) (Shankar & Sharma 2022). The practical utility of AI and multi-omics integration is exemplified by the discovery of previously hidden novel bioactive metabolites. For instance, genome mining and in silico approaches enabled the identification of Asperterpenoids A and B from the endophytic fungus *Aspergillus terreus*, which exhibit potent BACE1 inhibitory activity (Qi *et al.* 2016). Similarly, recent deep-mining strategies have linked cryptic biosynthetic gene clusters to novel chemical scaffolds across fungal taxa, highlighting the potential of AI to shift natural product discovery toward a more predictive and targeted paradigm (Shishodia *et al.* 2025) (Fig. 1 & 2, Table 1).

PREDICTING METABOLITE STRUCTURE AND BIOLOGICAL ACTIVITY IN FUNGAL ENDOPHYTES

Models based on artificial intelligence that identify epigenetic marks, transcription factor binding sites, and promoter elements which regulate clusters of genes that are quiescent or lowly expressed are also offered (Riedling, Walker & Rokas 2024; Wang & Mao 2025). Genome mining and screening show the presence of a secondary metabolite production in the endophytic fungus *Dactylonectria alcacerensis* CT-6 (Ming *et al.* 2023). Network-based prioritization systems have advanced past just detection using genome-mining tools, e.g. antiSMASH, MIBiG, and PRISM (Ming *et al.* 2023; Wang *et al.* 2025; Liu *et al.* 2021) (Fig. 1 & 2, Table 1). Unlike traditional rule-based methods that often overlook silent clusters, these AI-driven platforms offer significantly higher sensitivity by recognizing deep patterns in fragmented metagenomic data. Besides simple detection,

these models are now capable of predicting core chemical scaffolds and estimating biological activities through automated docking and scoring functions. They do this using scoring methods that consider biosynthetic feasibility, expected pharmacological potential, and structural originality (Kumari *et al.* 2025). These AI-generated molecular structures are subjected to in silico docking simulations against a range of biological targets, such as kinases, viral proteases, and oncogenic receptors, enabling high-throughput virtual screening procedures (Munshi *et al.* 2022). Docking research supports the idea that soybean-associated endophytic fungus could be a source of anti-COVID-19 metabolites (El-Hawary *et al.* 2021). Bayesian inference models and graph neural networks (GNNs) are increasingly being used to describe gene co-expression patterns and metabolite pathway interactions (Pöttker *et al.* 2023) (Fig. 1 & 2, Table 1). This ranks BGCs according to their likelihood of producing bioactive compounds and gives functional context. Further enhancements are the selection of possible clusters for use in chemical profiling, synthetic biology, heterologous expression, and other downstream applications (Hyde *et al.* 2024; Prakash *et al.* 2025; Shankar & Sharma 2022). These prediction filters aid in focusing downstream efforts on the most promising candidates by early exclusion of substances with significant cytotoxicity or poor pharmacokinetic characteristics (Wen *et al.* 2022). AI-driven methods would speed up drug discovery from endophytes by bridging the gap between expected biosynthetic capacity and empirically proven secondary metabolite production, as endophytic fungi are underrepresented in genomic databases (Kalita *et al.* 2025). This lack of comprehensive genomic data creates a significant 'knowledge gap', making it difficult for AI models to accurately distinguish between rare endophytic BGCs and common soil-dwelling fungal clusters. Furthermore, without a diverse reference library, many unique metabolic pathways remain 'dark' or unannotated, limiting the potential for discovering truly novel bioactive compounds. Addressing this gap through large-scale sequencing of diverse endophytic taxa is essential to improve the predictive accuracy of future AI-driven discovery pipelines.

AI IN ENDOPHYTIC FUNGAL FERMENTATION AND EXPRESSION OPTIMIZATION

Under typical laboratory conditions, many fungal endophyte biosynthetic gene clusters (BGCs) do not exhibit transcriptional activity (Yang *et al.* 2019). AI-driven culture models increase metabolite expression by optimizing growth parameters, providing potent treatments (Garg *et al.* 2025). The most efficient mixtures of carbon sources, micronutrients, pH, temperature, and co-culture combinations, such as the presence of host plant tissues or other microorganisms, are determined using the methods of multi-objective evolutionary algorithms and Bayesian optimization, which subsequently leads to the activation of biosynthetic gene clusters (Bode 2002; Li *et al.* 2021) (Fig. 1 & 2, Table 1). AI-based algorithms efficiently handle such complex variable interactions, unlike traditional one-factor-at-a-time (He *et al.* 2019; Liu *et al.* 2025). Lab-on-a-chip systems that generate real-time sensor data are connected to more advanced bioprocessing systems to provide reinforcement learning models, which subsequently dynamically regulate fermentation parameters (Aghdam & Brown 2021; Megnidio-Tchoukouegno, Gueguim Kana & Bancolé 2022). Based on the existing information, including genomic data of the host plant, fungal metabolic profiles, and known signalling molecules involved in plant-microbe interactions, predictive machine-learning models can detect the endophytic colonization of rice cultivar tissues with isolates of *Beauveria bassiana* and evaluate their possibility to be used as bio-controlling agents against the rice stem borer (Megnidio-Tchoukouegno, Gueguim Kana & Bancolé 2022). It has been established that fungal endophytes with the ability to express silent biosynthetic gene clusters can be predictably induced and that the production of metabolites can be greatly enhanced by adaptive control methods that adjust cultivation conditions to metabolic production (Pillay *et al.* 2022). Lastly, while co-expression analysis is a fundamental statistical approach, when integrated with AI-driven regulatory network modelling, it reveals deeper insights into fungal pathogenicity. For instance, studies show that the PacC transcription factor could be a factor in the pathogenicity of the Chinese hickory in the presence of the transcription factor, which is known as *Botryosphaeria dothidea* (Liang *et al.* 2025) (Fig. 1 & 2, Table 1).

COMBINING AI AND MULTI-OMICS TO ACTIVATE FUNGAL ENDOPHYTE PATHWAYS

Integrating multi-omics measurements with AI modelling is also necessary to unlock the entire metabolic potential of fungal endophytes (Shishodia *et al.* 2025; Liu *et al.* 2025) (Fig. 1 & 2, Table 1). By predicting which

BGCs are epigenetically repressed, models trained on epigenetic data such as histone modification maps, DNA methylation profiles, and RNA-seq expression levels can direct focused activation (Moore, Le & Fan 2013; Al Aboud, Tupper & Jialal 2023; Chen *et al.* 2023; Varghese, Rajeshkumar & Jisha 2025) (Fig. 1 & 2, Table 1). For instance, regulatory elements governing BGC expression can be found using AI-assisted analysis of Chip-seq, ATAC-seq, and RNA-seq data (Carrión *et al.* 2019; Motalebnejad *et al.* 2025). These AI-driven discoveries of BGC regulatory elements directly inform the precision design of CRISPR-based gene activation systems (CRISPRi). By utilizing guide RNAs targeted to the AI-identified epigenetic 'hotspots' (Aghdam & Brown 2021; Chowdhary, Arora & Sharma 2022; Zhao *et al.* 2024), researchers can precisely modify metabolic pathways to induce the expression of silent gene clusters. This targeted activation provides the high-quality, validated experimental data required to feed back into deep multimodal AI frameworks, which integrate transcriptomic, proteomic, and metabolomic data to show how external signals, such as cues derived from the plant host and internal cellular networks, interact to control secondary metabolism in endophytes (Yuan *et al.* 2019; Chen *et al.* 2022). To create logical plans to control metabolite production in plants and in vitro, these integrative methods are essential as they transition fungal biotechnology from traditional trial-and-error discovery to a predictive, design-driven science. By bridging the gap between computational BGC prioritization and experimental validation through CRISPRi, these frameworks enable the sustainable large-scale production of high-value fungal metabolites, ultimately accelerating the drug discovery pipeline for novel antimicrobials and anticancer agents (Jha *et al.* 2023).

AI MEETS ECOSYSTEMS IN FUNGAL ENDOPHYTE DISCOVERY

Fungal regulatory genetics and environmental modelling are combined in the new field of coelomic to clarify how natural stresses affect secondary metabolism (Tiwari, Adil & Park 2025; Tiwari & Bae 2022). AI models, especially deep neural networks and ensemble techniques like decision trees, anticipate environmentally inducible BGCs in fungal endophytes by simulating abiotic challenges, including salinity, drought, and temperature fluctuations. (Zhang *et al.* 2024). The predictions thus allow for the formulation of in situ mimetic studies that replicate ecological triggers in laboratories (Kaur *et al.* 2024). These approaches provide essential knowledge and highlight new opportunities and challenges in natural product drug discovery from endophytic fungi (Tiwari, Adil & Park 2022) (Fig. 1 & 2, Table 1).

COMPELLING CASE EXAMPLES IN AI-DRIVEN ENDOPHYTE APPLICATIONS

AI is already demonstrating substantial practical value across fungal endophyte research pipelines (Kunwar *et al.* 2023). In anticancer drug discovery, deep learning platforms have screened thousands of predicted fungal metabolites against breast cancer receptor targets, efficiently prioritizing candidates based on predicted bioactivity, selectivity, and toxicity profiles (Varghese *et al.* 2024). In agriculture, Random Forest and Gradient Boosting machine learning models identified *Beauveria bassiana* strains with enhanced colonization ability in rice under heat stress (Megnidio-Tchoukouegno, Gueguim Kana & Bancole 2022). Importantly, AI tools are addressing challenges posed by unculturable fungi by mining early metagenomic sequences to predict cryptic BGCs. These predictions are primarily based on conserved biosynthetic motifs and structural patterns recognized by deep learning models from established BGC databases. Since these mushrooms are non-cultivable, the 'ground truth' for evaluation is established through synthetic biology, where AI-predicted gene clusters are synthesized and expressed in well-characterized heterologous hosts. This functional expression serves as the critical reference point to validate whether the predicted BGCs are indeed capable of producing the expected chemical diversity (Figueiredo *et al.* 2025) (Fig. 1 & 2, Table 1).

ETHICAL, REGULATORY, AND PRACTICAL FRAMEWORK FOR AI-GUIDED FUNGAL ENDOPHYTES RESEARCH

As AI accelerates fungal endophyte bioprospecting, strict adherence to ethical and regulatory frameworks is essential (Gupta & Kumar, 2024). Compliance with the Nagoya Protocol and Access and Benefit-Sharing (ABS) agreements ensures the equitable use of microbial genetic resources, particularly those derived from biodiversity-rich or indigenous territories (Sharma *et al.* 2018). Embracing FAIR data principles (Findable, Accessible, Interoperable, and Reusable) fosters transparency, reproducibility, and collaborative progress in AI-assisted discovery (González-Rodríguez *et al.* 2024). Moreover, forming partnerships with local scientists,

indigenous communities, and conservation organizations ensures that AI-enabled research advances both scientific innovation and socio-environmental stewardship. Such coordination is paramount to ensuring equitable benefit-sharing, where pharmacological discoveries derived from traditional ecological knowledge are co-developed with local stakeholders. This inclusive approach not only strengthens the accuracy of AI models by integrating site-specific environmental data but also protects the sovereignty of biological resources, aligning bioprospecting with sustainable and ethical frameworks (Tella *et al.* 2025) (Table 1).

CONCLUSION

The integration of artificial intelligence (AI) with multi-omics technologies has ushered in a new era of drug discovery from fungal endophytes. By overcoming the challenge of silent BGCs through advanced genome mining, predictive modelling, and epigenetic manipulation, AI enables the systematic exploration of previously inaccessible metabolic diversity. Machine learning and deep learning tools enhance BGC annotation, metabolite structure prediction, and bioactivity profiling, while AI-driven fermentation optimization and multi-omics integration unlock novel pathways. Additionally, coelomic provides insights into environmental regulation of fungal metabolism, guiding targeted activation strategies. Real-world applications in drug discovery and agriculture highlight AI's transformative potential, though ethical and regulatory considerations must remain central to bioprospecting efforts. Moving forward, the synergy between AI, synthetic biology, and functional validation will be crucial in harnessing fungal endophytes as a sustainable source of next-generation therapeutics. This interdisciplinary approach not only accelerates natural product discovery but also ensures that scientific advancements align with ecological and ethical stewardship.

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DECLARATION OF CONFLICT OF INTEREST

Regarding the publication of this review, the authors affirm that they have no conflicts of interest.

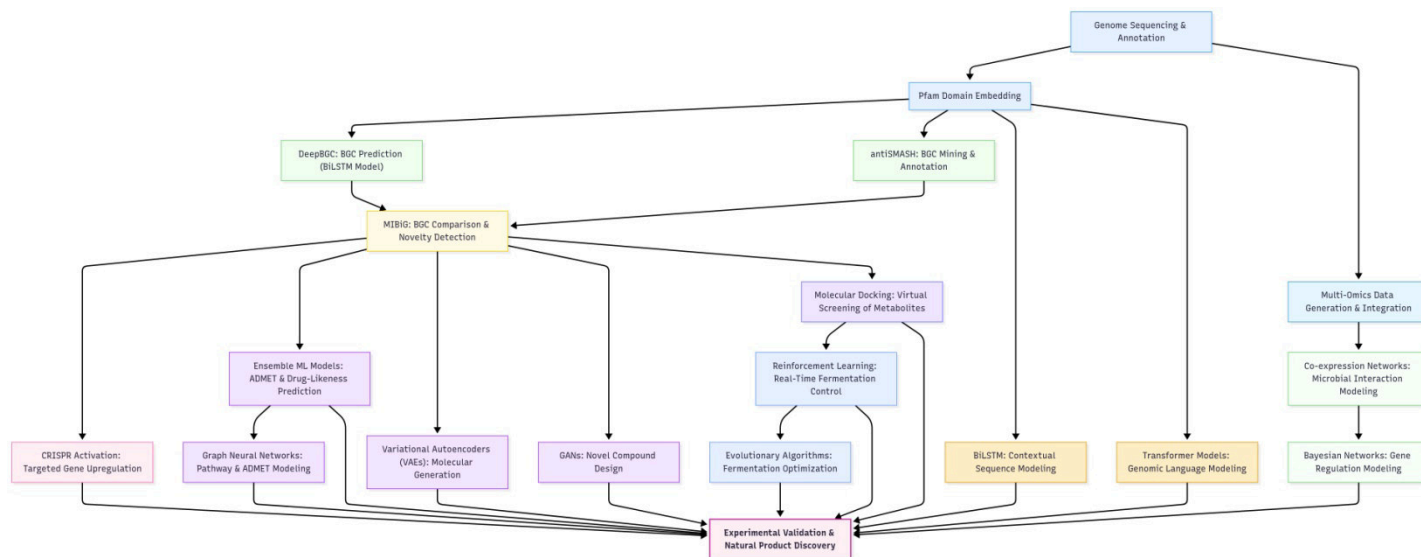


Figure 1 (above). The workflow for the study and the logical relationships between the several experimental or data processing procedures are depicted in this flowchart. Boxes stand for significant stages or analytical points, whereas arrows illustrate the development, interdependencies, and integration of results.

Figures 2i to 2vi (below). The figures represent multiple panels (AI-A6, BI-B7, and CI-C3), each representing distinct outcomes or experimental conditions in the study. Each panel's size is standardized to ensure consistent comparison. The arrangement allows for comprehensive visualization and facilitates the identification of key differences across the tested variables. Panel labels correspond to the different categories or treatments evaluated and are clearly marked for easy reference in the main text.

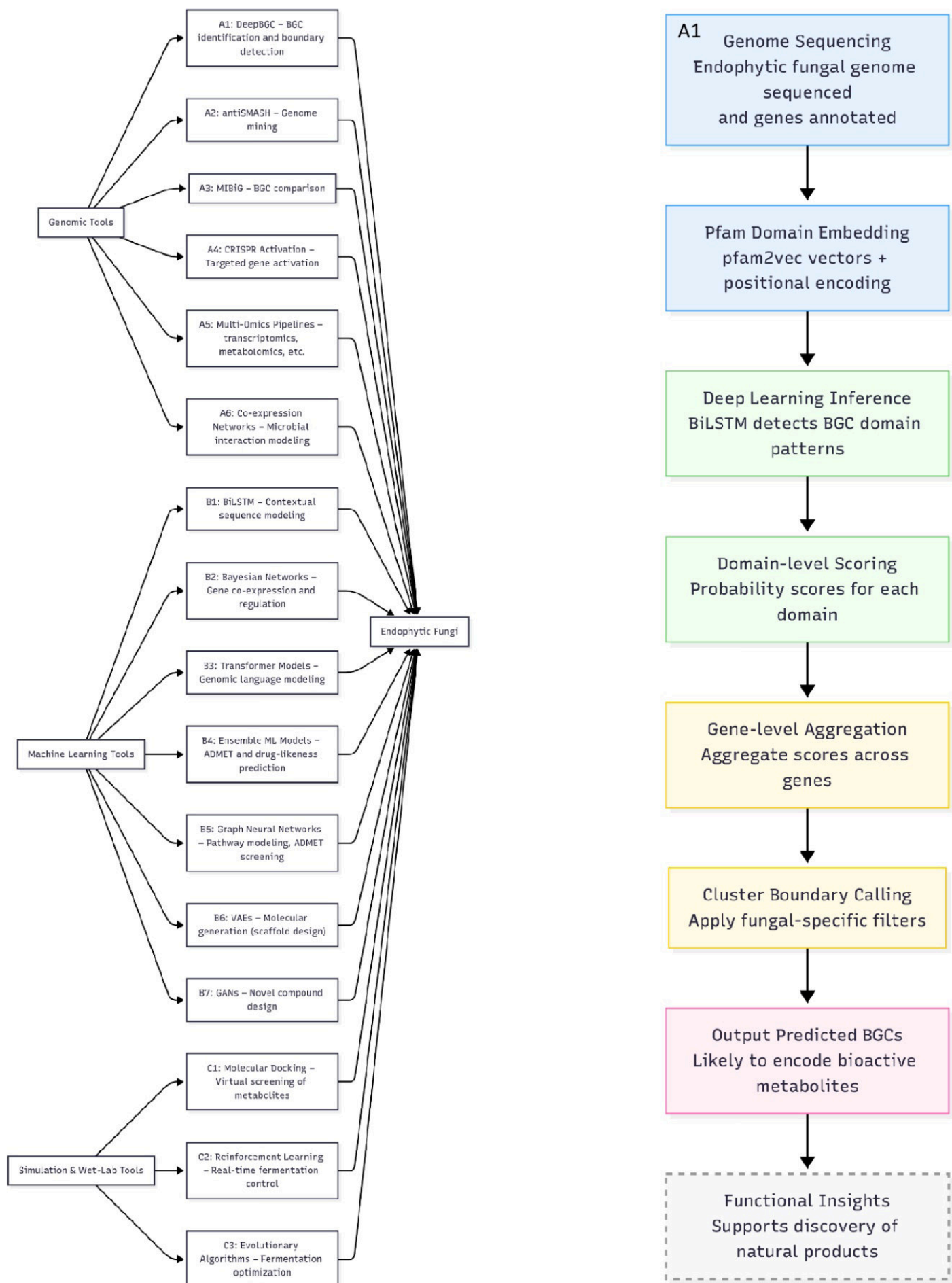


Fig. 2i

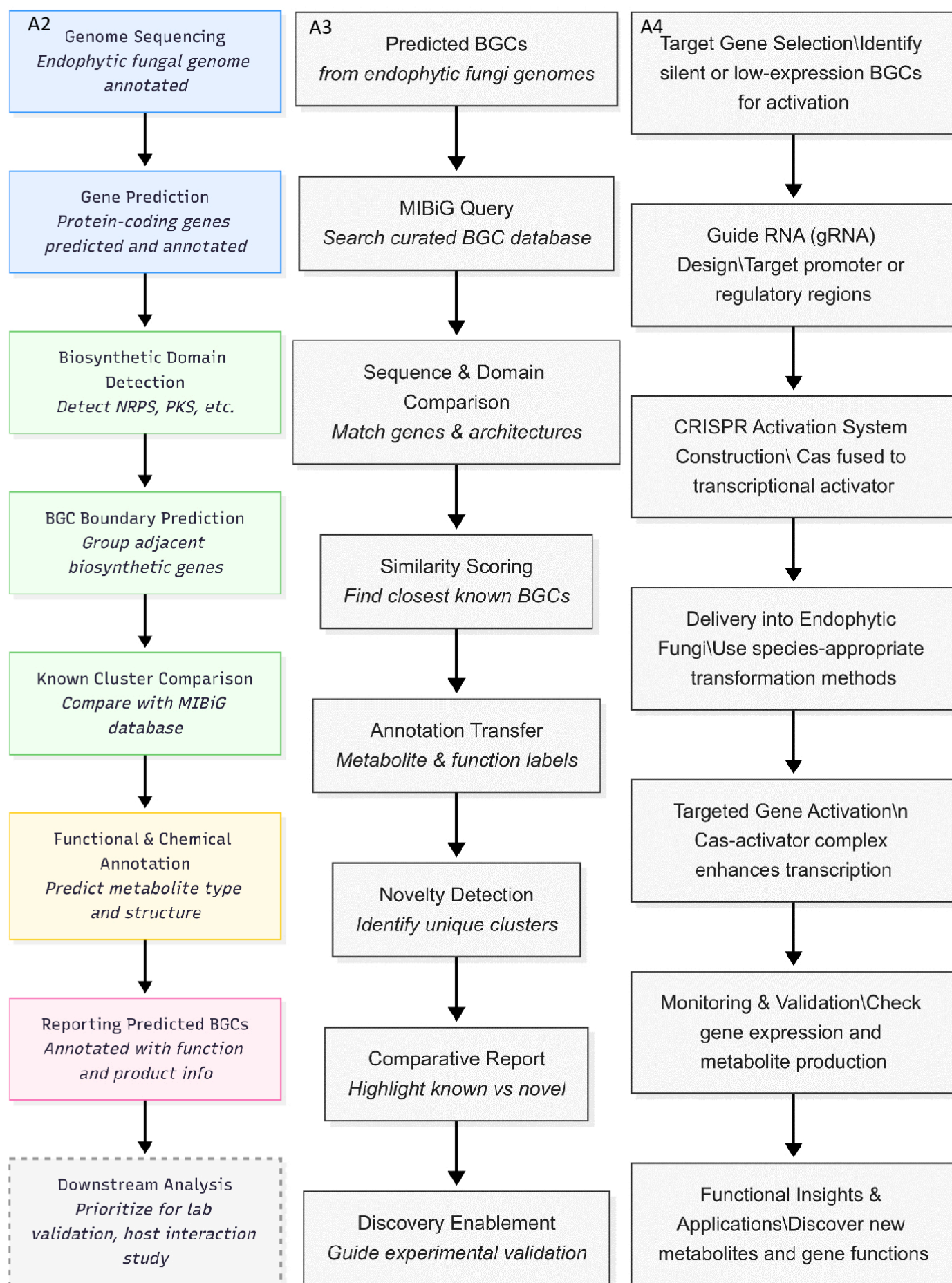


Fig. 2ii

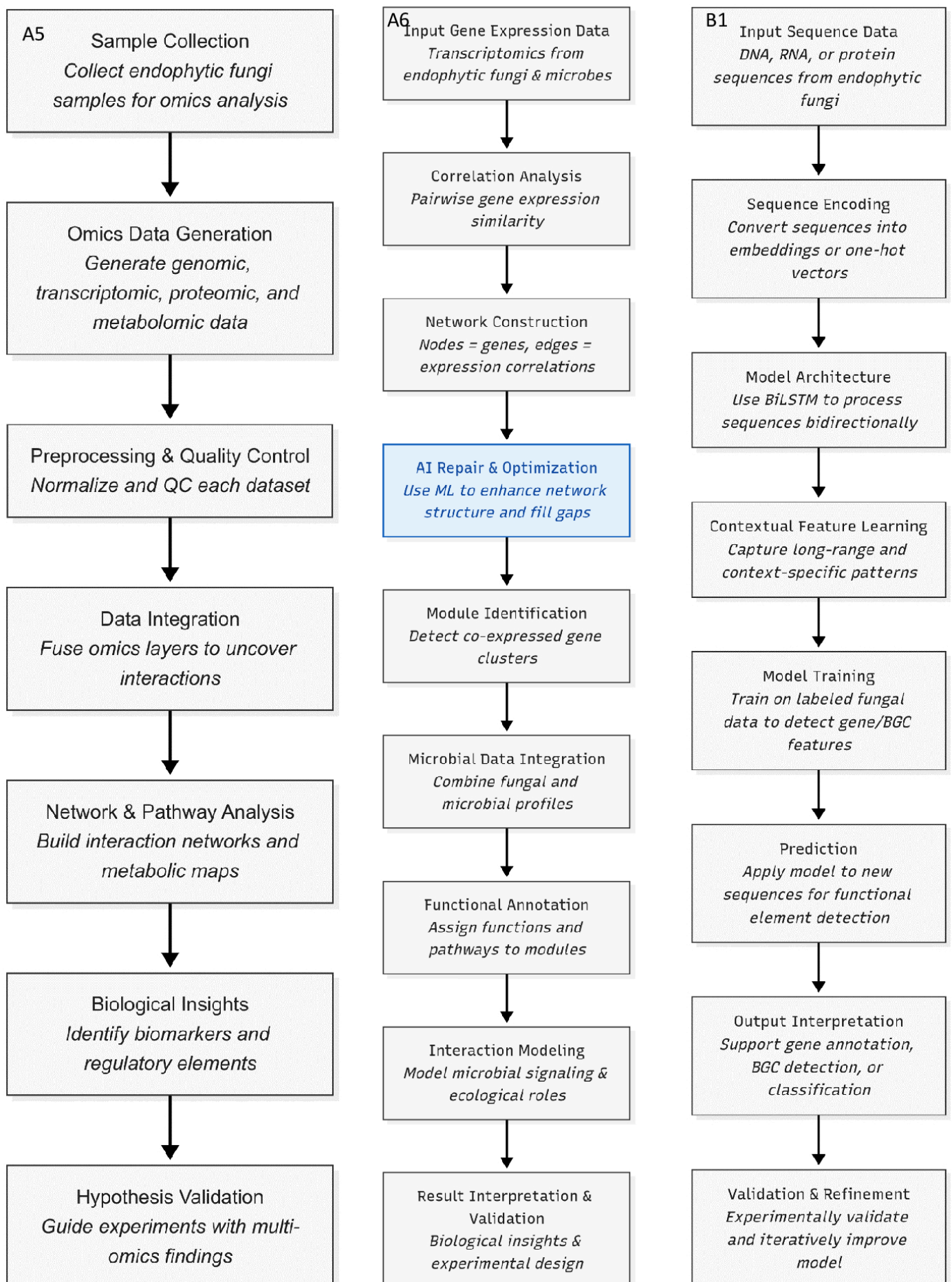


Fig. 2iii

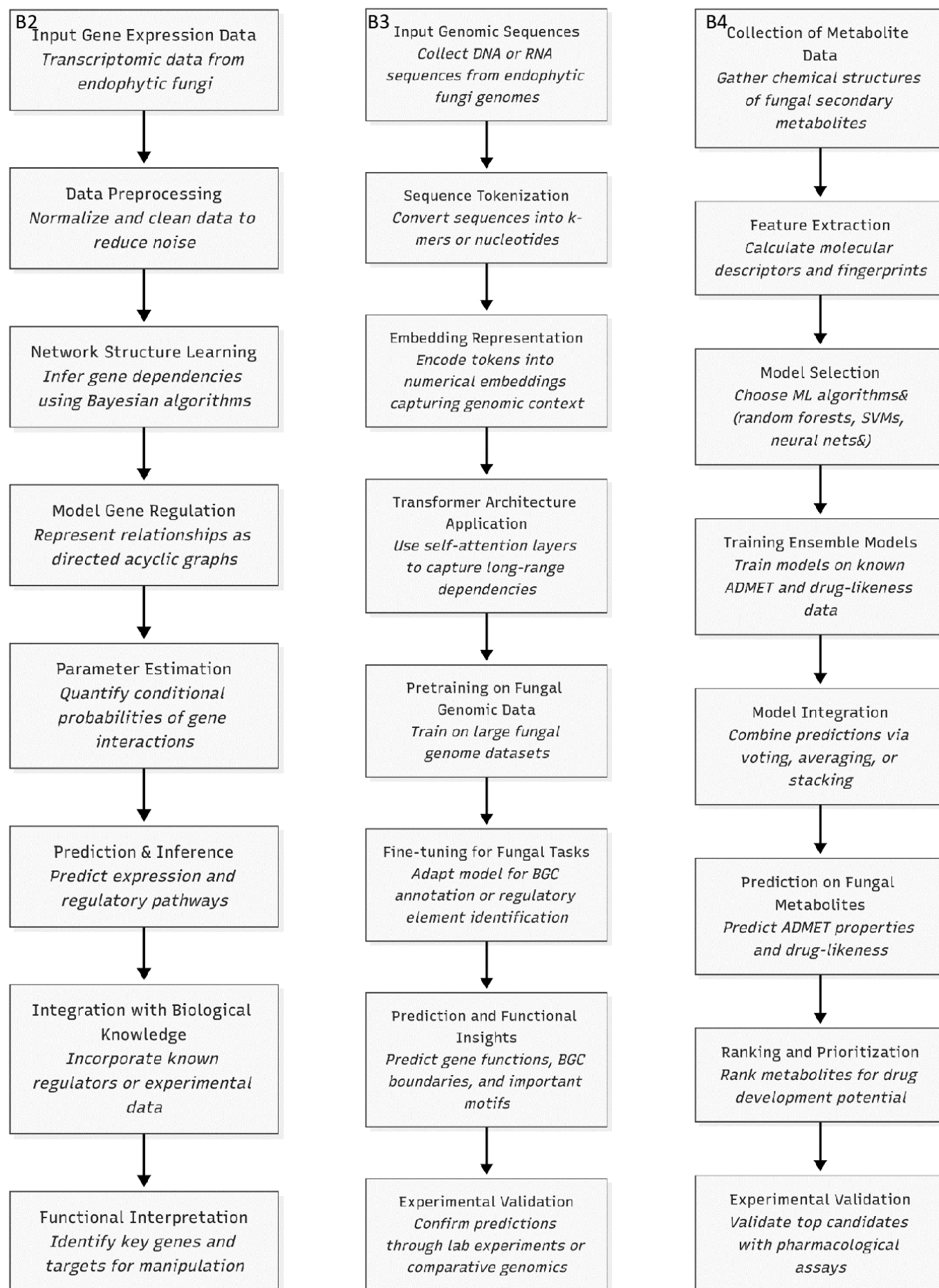


Fig. 2iv

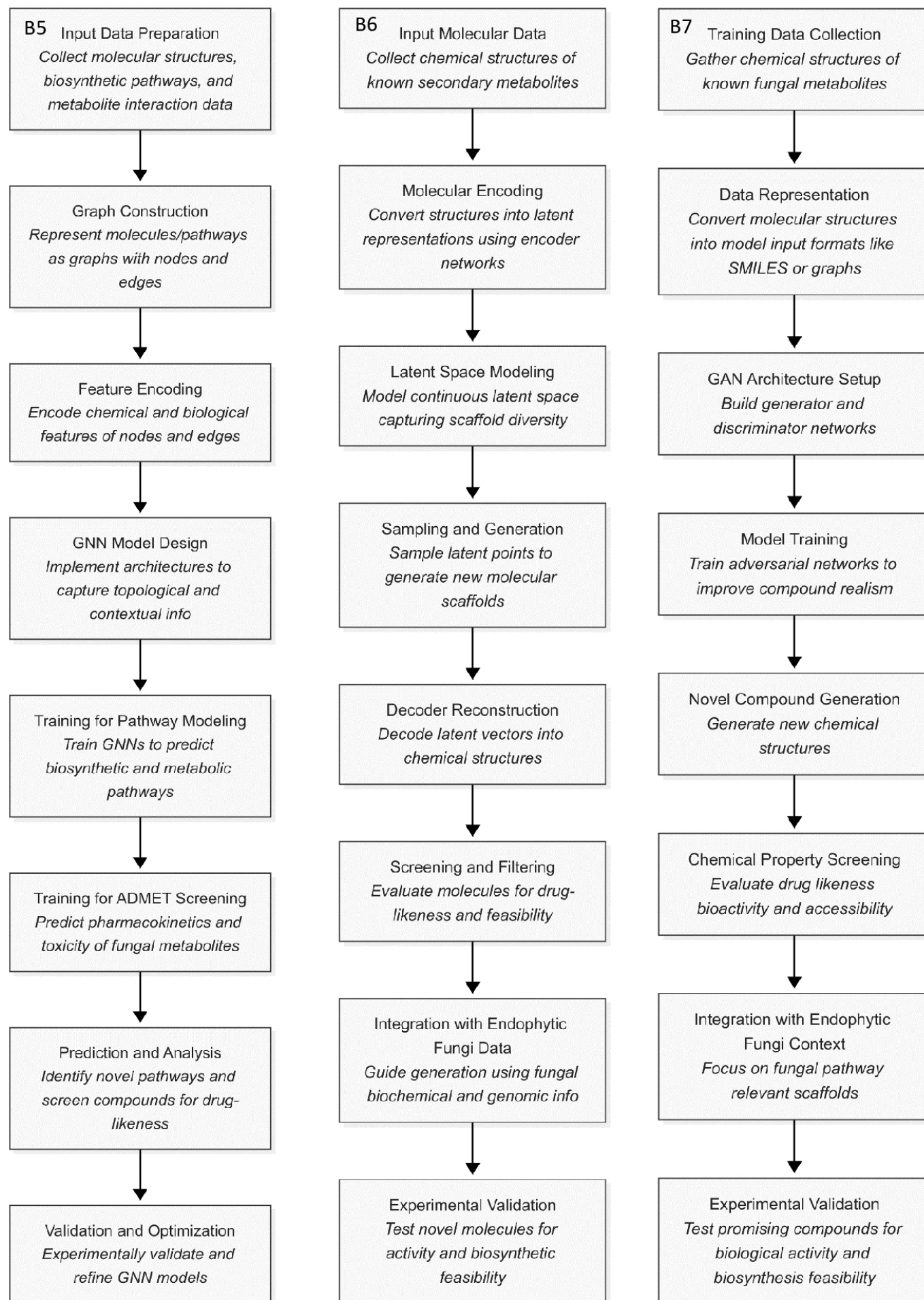


Fig. 2v

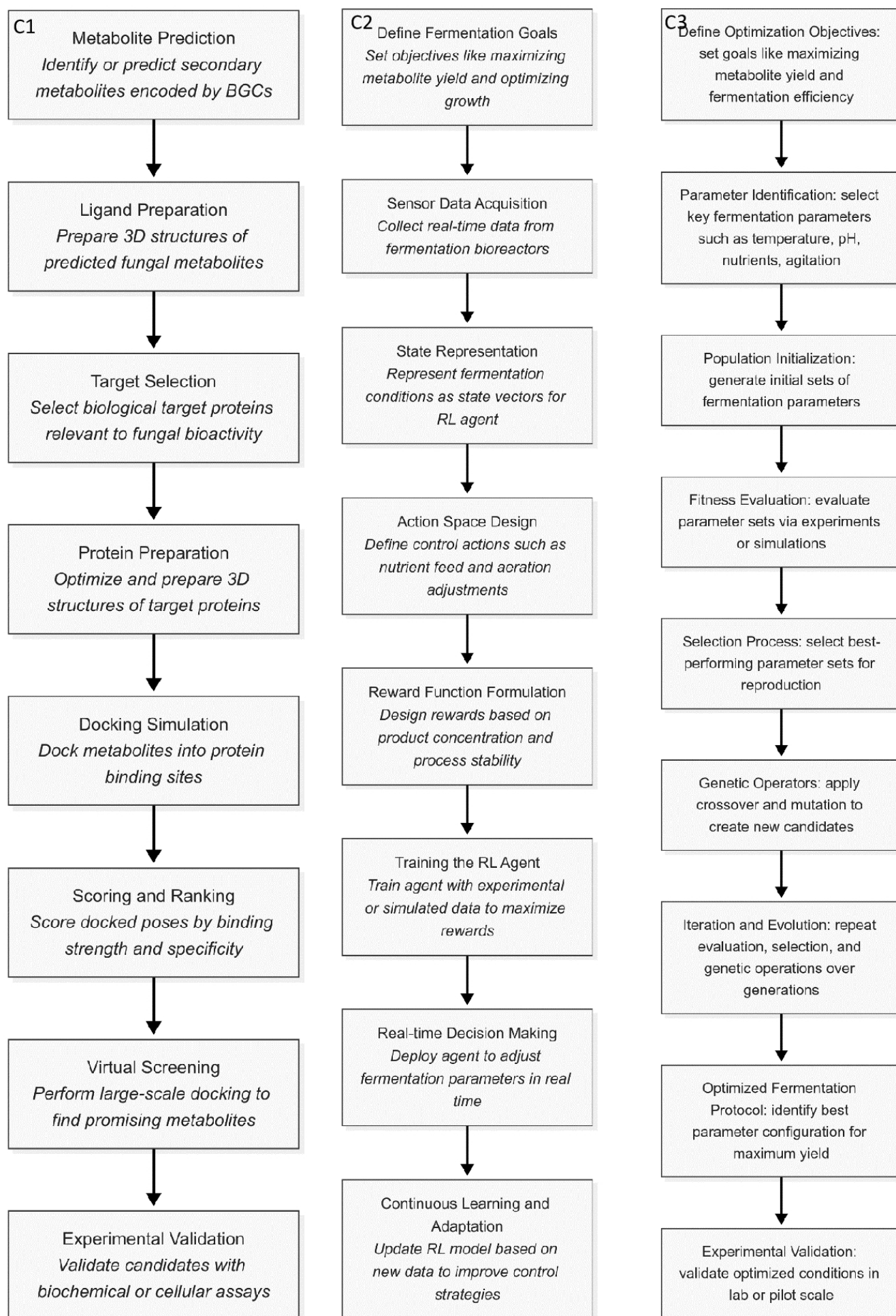


Fig. 2vi

Tool / Model	Application	Use Case / Output	References
DeepBGC (CNN-based)	BGC identification and boundary detection	Detects cryptic biosynthetic gene clusters in fungal genomes	Hannigan <i>et al.</i> 2019
antiSMASH	Genome mining	Annotates known and novel BGCs from genomic sequences	Liu <i>et al.</i> 2021
MIBiG	Reference database for BGC comparison	Matches BGCs with characterized clusters and known metabolites	Ming <i>et al.</i> 2023
BiLSTM (Bidirectional LSTM)	Contextual sequence modelling	Predicts long-range dependencies in regulatory DNA sequences	Tiwari & Bae 2022
Transformer Models (e.g., BERT)	Genomic language modelling	Identifies regulatory motifs and transcription factor binding sites	Yu <i>et al.</i> 2024
Graph Neural Networks (GNNs)	Pathway modelling, ADMET screening	Models gene-gene interactions, pharmacokinetics, and toxicology	Pöttker <i>et al.</i> 2023
Bayesian Networks	Gene co-expression and regulation	Predicts gene interactions under variable environmental conditions	Montero-Vargas <i>et al.</i> 2020
Variational Autoencoders (VAEs)	Molecular generation	Designs novel metabolite scaffolds based on learned chemical features	Roy <i>et al.</i> 2025
Generative Adversarial Networks (GANs)	Synthetic compound generation	Creates synthetic compound structures mimicking real metabolite scaffolds	Wang <i>et al.</i> 2022
Molecular Docking Algorithms	Virtual screening	Assesses binding affinity of predicted metabolites to disease-related proteins	El-Hawary <i>et al.</i> 2021
Ensemble ML Models	Drug-likeness prediction	Filters out cytotoxic or poorly absorbed drug candidates (ADMET profiling)	Chen <i>et al.</i> 2023
Evolutionary Algorithms	Fermentation optimization	Determines ideal culture conditions for optimal metabolite production	Li <i>et al.</i> 2021
Reinforcement Learning (RL)	Real-time bioprocess control	Adjusts fermentation parameters (pH, temperature) based on sensor feedback	Megnidio-Tchoukouegno <i>et al.</i> 2022
CRISPR Activation Systems	Targeted gene activation	Enables precise BGC regulation via gRNA-guided transcriptional tuning	Chowdhary <i>et al.</i> 2022; Zhao <i>et al.</i> 2024
Multi-Omics Integration Pipelines	Data fusion (transcriptomics, metabolomics, etc.)	Models comprehensive regulation of metabolic pathways	Shankar & Sharma 2022
Co-expression Network Analysis	Microbial interaction modelling	Predicts inter-kingdom signalling (e.g., quorum sensing) affecting BGC dynamics	Liang <i>et al.</i> 2025

Table 1. Artificial Intelligence Tools and Techniques in Fungal Endophytes Research

REFERENCES

- Adeleke, BS; Babalola, OO (2021) Pharmacological potential of fungal endophytes associated with medicinal plants: a review. *Journal of Fungi* **7**(2), 147
<https://doi.org/10.3390/jof7020147>
- Aghdam, SA; Brown, AMV (2021) Deep learning approaches for natural product discovery from plant endophytic microbiomes. *Environmental Microbiome* **16**(1), 6
<https://doi.org/10.1186/s40793-021-00375-0>
- Al Aboud, NM; Tupper C; Jialal I (2023) Genetics, epigenetic mechanism. [Updated 2023 Aug 14]. In: StatPearls [Internet]. Treasure Island (FL): StatPearls Publishing.
<https://www.ncbi.nlm.nih.gov/books/NBK532999/>
- Al Shami, R; Mousa, WK (2026) Mining the Hidden Pharmacopeia: Fungal Endophytes, Natural Products, and the Rise of AI-Driven Drug Discovery. *International Journal of Molecular Sciences* **27**(3):1365
<https://doi.org/10.3390/ijms27031365>
- Ali, MA; Ahmed, T; Ibrahim, E; Rizwan, M; Chong, KP; Yong, JWH (2024) A review on mechanisms and prospects of endophytic bacteria in biocontrol of plant pathogenic fungi and their plant growth-promoting activities. *Heliyon* **10**(11):e31573

- <https://doi.org/10.1016/j.heliyon.2024.e31573>
- Bhardwaj, M; Kailoo, S; Khan, RT; Khan, SS; Rasool, S (2023) Harnessing fungal endophytes for natural management: a biocontrol perspective. *Frontiers in Microbiology* **14**:1280258
<https://doi.org/10.3389/fmicb.2023.1280258>
- Bode, HB; Bethe, B; Höfs, R; Zeeck, A (2002) Big effects from small changes: possible ways to explore nature's chemical diversity. *Chembiochem* **3**(7):619–27
[https://doi.org/10.1002/1439-7633\(20020703\)3:7<619::AID-CBIC619>3.0.CO;2-9](https://doi.org/10.1002/1439-7633(20020703)3:7<619::AID-CBIC619>3.0.CO;2-9)
- Carrión, VJ; Perez-Jaramillo, J; Cordovez, V; Tracanna, V; de Hollander, M; Ruiz-Buck, D; Mendes, LW; van Ijcken, WFJ; Gomez-Exposito, R; Elsayed, SS; Mohanraju, P; Arifah, A; van der Oost, J; Paulson, JN; Mendes, R; van Wezel, GP; Medema, MH; Raaijmakers, JM (2019) Pathogen-induced activation of disease-suppressive functions in the endophytic root microbiome. *Science* **366**(6465):606–612
<https://doi.org/10.1126/science.aaw9285>
- Chen, YP; Su, PW; Stadler, M; Xiang, R; Hyde, KD; Tian, WH; Maharachchikumbura, SSN (2023) Beyond observation: genomic traits and machine learning algorithms for predicting fungal lifestyles. *Mycosphere* **14**(1):1530–1563
<https://doi.org/10.5943/mycosphere/14/1/17>
- Chen, XL; Sun, MC; Chong, SL; Si, JP; Wu, LS (2022) Transcriptomic and metabolomic approaches deepen our knowledge of plant–endophyte interactions. *Frontiers in Plant Science* **12**:700200
<https://doi.org/10.3389/fpls.2021.700200>
- Chowdhary, K; Arora, H; Sharma, S (2022). CRISPR/Cas9-based genome editing as a way ahead for inducing production of bioactive metabolites in endophytes. *National Academy Science Letters* **45**(3):275–280
<https://doi.org/10.1007/s40009-022-01107-9>
- El-Hawary, SS; Mohammed, R; Bahr, HS; Attia, EZ; El-Katatny, MH; Abelyan, N; Al-Sanea, MM; Moawad, AS; Abdelmohsen, UR (2021) Soybean-associated endophytic fungi as potential source for anti-COVID-19 metabolites supported by docking analysis. *Journal of Applied Microbiology* **131**(3):1193–1211
<https://doi.org/10.1111/jam.15031>
- Figueiredo, G; Osório, H; Mendes, MV; Mendo, S (2025) A review on the expanding biotechnological frontier of *Pedobacter*. *Biotechnology Advances* **82**, 108588
<https://doi.org/10.1016/j.biotechadv.2025.108588>
- Gakuubi, MM; Munusamy, M; Liang, ZX; Ng, SB (2021). Fungal endophytes: a promising frontier for discovery of novel bioactive compounds. *Journal of Fungi* **7**(10), 786
<https://doi.org/10.3390/jof7100786>
- Garg, S; Kim, M; Romero-Suarez, D (2025) Current advancements in fungal engineering technologies for Sustainable Development Goals. *Trends in Microbiology* **33**(3):285–301
<https://doi.org/10.1016/j.tim.2024.11.001>
- González-Rodríguez, VE; Izquierdo-Bueno, I; Cantoral, JM; Carbú, M; Garrido, C (2024) Artificial Intelligence: a promising tool for application in phytopathology. *Horticulturae* **10**, 197
<https://doi.org/10.3390/horticulturae10030197>
- Gupta, S; Kulkarni, MG; White, JF; Van Staden, J (2020) Epigenetic-based developments in the field of plant endophytic fungi. *South African Journal of Botany* **134**:394–400
<https://doi.org/10.1016/j.sajb.2020.07.019>
- Gupta, S; Kumar, D (2024) Driven bioprospecting of microbial resources. In: Gupta, S; Kumar, D; Negi, R; Singh, R; Ansari, MJ; Kashyap, S; Mehrotra S (Eds.). *Genomic Intelligence: Metagenomics and Artificial Intelligence* (1st ed.). (pp. 257–275) CRC Press
<https://www.taylorfrancis.com/chapters/edit/10.1201/9781003570233-16/ai-driven-bioprospecting-microbial-resources-sheetanshu-gupta-dhirendra-kumar>

- Hannigan, GD; Prihoda, D; Palicka, A; Soukup, J; Klempir, O; Rampula, L; Durcak, J; Wurst, M; Kotowski, J; Chang, D; Wang, R; Piizzi, G; Temesi, G; Hazuda DJ; Woelk, CH (2019) A deep learning genome-mining strategy for biosynthetic gene cluster prediction. *Nucleic acids research* **47**(18):e110
<https://doi.org/10.1093/nar/gkz654>
- Hashem, AH; Attia, MS; Kandil, EK; Fawzi, MM; Abdelrahman, AS; Khader, MS; Khodaira, MA; Emam, AE; Goma, MA; Abdelaziz, AM (2023) Bioactive compounds and biomedical applications of endophytic fungi: a recent review. *Microbial Cell Factories* **22**(1), 107
<https://doi.org/10.1186/s12934-023-02118-x>
- He, C; Wang, W; Hou, J (2019) Characterization of dark septate endophytic fungi and improve the performance of liquorice under organic residue treatment. *Frontiers in Microbiology* **10**, 1364
<https://doi.org/10.3389/fmicb.2019.01364>
- Hyde, KD; Baldrian, P; Chen, Y; Thilini Chethana, KW; De Hoog, S; Doilom, M; de Farias, ARG; Gonçalves, MFM; Gonkhom, D; Gui, H; Hilário, S; Hu, Y; Jayawardena, RS; Khyaju, S; Kirk, PM; Kohout, P; Luangharn, T; Maharachchikumbura, SSN; Manawasinghe, IS; Mortimer, PE; Niego, AG; Phonemany, M; Sandargo, B; Senanayake, IC; Stadler, M; Surup, F; Thongklang, N; Wanasinghe, DN; Bahkali, AH; Walker, A (2024) Current trends, limitations and future research in the fungi? *Fungal Diversity* **125**(1):1–71
<https://doi.org/10.1007/s13225-023-00532-5>
- Jha, P; Kaur, T; Chhabra, I; Panja, A; Paul, S; Kumar, V; Malik, T (2023) Endophytic fungi: hidden treasure chest of antimicrobial metabolites interrelationship of endophytes and metabolites. *Frontiers in Microbiology* **14**:1227830
<https://doi.org/10.3389/fmicb.2023.1227830>
- Kalita, I; Bhattacharjee, S; Saharia, M (2025) Advancements in medicinal plant research. harnessing artificial intelligence, machine learning, deep learning, and bioinformatics. In: Chen, J-T (Eds.) *Biotechnology, Multiple Omics, and Precision Breeding in Medicinal Plants* (pp. 135–145). CRC Press
<http://dx.doi.org/10.1201/9781003475491-11>
- Kalyanaraman, R; Narasimhan, B; Venkatesan, N; Sudharsan, MS (2025). Marine algal-derived endophytic fungi: secondary metabolites and applications. In: Abd-Elsalam, KA; AbuQamar, SF (Eds.), *Fungal Endophytes* **1**:107–132. Springer, Singapore.
https://doi.org/10.1007/978-981-97-7312-1_6
- Kaur, R; Kaur, C; Kaur, G; Kaur, J; Rath, SK; Dwibedi, V (2024) From microscopy to omics: a comprehensive review of tools and techniques in studying endophytic adaptation under abiotic and biotic stress. *Journal of Plant Growth Regulation* **44**: 6766–6784
<https://doi.org/10.1007/s00344-024-11323-w>
- Kumari, S; Jain, A; Kaur, G; Jain, S (2025) Big data and machine learning in endophytic drug discovery: Accelerating innovations. In: Dwibedi, V; Kapoor, N; Gambhir, L; Kajale, S (Eds.) *Navigating Endophytic Research for Next-Generation Therapeutics* (pages 441–462). Academic Press
<https://doi.org/10.1016/B978-0-443-31484-1.00022-0>
- Kunwar, S; Joshi, A; Gururani, P; Pandey, D; Pandey, N (2023) Physiological and AI-based study of endophytes on medicinal plants: A mini review. *Plant Science Today* **10**(sp2):53–60
<https://doi.org/10.14719/pst.2555>
- Li, H., Dou, M., Wang, X., Guo, N., Kou, P., Jiao, J., & Fu, Y. (2021). Optimization of cellulase production by a novel endophytic fungus *Penicillium oxalicum* R4 isolated from *Taxus cuspidata*. *Sustainability* **13**(11), 6006
<https://doi.org/10.3390/su13116006>
- Liang, D; Jiang, Y; Ai, W; Zhang, Y; Mao, C; Ma, T; Zhang, C (2025) Co-expression network analysis suggests PacC transcriptional factor involved in *Botryosphaeria dothidea* pathogenicity in Chinese hickory. *Journal of Fungi* **11**(8), 580
<https://doi.org/10.3390/jof11080580>

- Liu, R; Peng, X-P; Newman, DJ; Purchase, D; Li, G; Kusari, S (2025) Unlocking the metabolic potential of endophytic fungi through epigenetics: a paradigm shift for natural product discovery and plant–microbe interactions. *Natural Product Reports* **42**(10):1690–1716
<https://doi.org/10.1039/D5NP00028A>
- Liu, X; Zhou, Z-Y; Cui, J-L; Wang, M-L; Wang, J-H (2021) Biotransformation ability of endophytic fungi: from species evolution to industrial applications. *Applied Microbiology and Biotechnology* **105**(19):7095–7113
<https://doi.org/10.1007/s00253-021-11554-x>
- Liu, Y; Xu, M; Tang, Y; Shao, Y; Wang, H; Zhang, H (2022) Genome features and antiSMASH analysis of an endophytic strain *Fusarium* sp. R1. *Metabolites* **12**(6), 521
<https://doi.org/10.3390/metabo12060521>
- Mansourvar, M; Charylo, KR; Frandsen, RJN; Brewer, SS; Hoof, JB (2025) Automated fungal identification with deep learning on time-lapse images. *Information* **16**(2), 109
<https://doi.org/10.3390/info16020109>
- Meenambiga, SS; Rajagopal, K (2018) Antibiofilm activity and molecular docking studies of bioactive secondary metabolites from endophytic fungus *Aspergillus nidulans* on oral *Candida albicans*. *Journal of Applied Pharmaceutical Science* **8**(3):37–45
<https://doi.org/10.7324/JAPS.2018.8306>
- Megnidio-Tchoukouegno, MM; Gueguim Kana, EB; Bancole, WBA (2022) Machine learning model to predict endophytic colonisation of rice cultivar plant tissues by *Beauveria bassiana* isolates and their potential as bio-control agents against rice stem borer using existing knowledge. *F1000Research* **11**, 1249
<https://doi.org/10.12688/f1000research.126479.1>
- Ming, Q; Huang, X; He, Y; Qin, L; Tang, Y; Liu, Y; Huang, Y; Zhang, H; Li, P (2023) Genome mining and screening for secondary metabolite production in the endophytic fungus *Dactylonectria alcacerensis* CT-6. *Microorganisms* **11**(4), 968
<https://doi.org/10.3390/microorganisms11040968>
- Montero-Vargas, M; Umaña-Jiménez, JC; Escudero-Leiva, E; Chaverri-Echandi, P (2020) Phylogenetic analysis of ITS data from Endophytic fungi using Massive Parallel Bayesian Tree Inference with ExaBayes. *Tecnología en Marcha*. Edición especial 2020. 6th Latin America High Performance Computing Conference (CARLA) **33**:74–79
<https://doi.org/10.18845/tm.v33i5.5079>
- Moore, L; Le, T; Fan, G (2013) DNA methylation and its basic function. *Neuropsychopharmacology* **38**(1):23–38
<https://doi.org/10.1038/npp.2012.112>
- Motallebnejad, P; Lee, Z; One, JL; Cichocki, F; Hu, W-S; Azarin, SM (2025) Integrated ATAC-seq and RNA-seq analysis identifies key regulatory elements in NK cells activated with feeder cells and IL-2. *Bioengineering & Translational Medicine* **10**(3):e10747
<https://doi.org/10.1002/btm2.10747>
- Munshi, M; Zilani, MNH; Islam, MA; Biswas, P; Das, A; Afroz, F; Hasan, MN (2022) Novel compounds from endophytic fungi of *Ceriops decandra* inhibit breast cancer cell growth through estrogen receptor alpha in in-silico study. *Informatics in Medicine Unlocked* **32**:101046
<https://doi.org/10.1016/j.imu.2022.101046>
- Pillay, LC; Nekati, L; Makhwitine, PJ; Ndlovu, SI (2022) Epigenetic activation of silent biosynthetic gene clusters in endophytic fungi using small molecular modifiers. *Frontiers in Microbiology* **13**:815008
<https://doi.org/10.3389/fmicb.2022.815008>
- Pöttker, M; Kiehl, K; Jarmer, T; Trautz, D (2023) Convolutional neural network maps plant communities in semi-natural grasslands using multispectral unmanned aerial vehicle imagery. *Remote Sensing* **15**(7), 1945
<https://doi.org/10.3390/rs15071945>
- Prakash, S; Kumari, H; Sinha, M; Kumar, A (2025) Regulation and induction of fungal secondary metabolites: A comprehensive review. *Archives of Microbiology* **207**(8):1–36
<https://doi.org/10.1007/s00203-025-04386-0>

- Qi, C; Bao, J; Wang, J; Zhu, H; Xue, Y; Wang, X; Li, H; Sun, W; Gao, W; Lai, Y; Chen, J-G; Zhang, Y (2016) Asperterpenes A and B, two unprecedented meroterpenoids from *Aspergillus terreus* with BACE1 inhibitory activities. *Chemical Science* **7**(10):6563–6572
<https://doi.org/10.1039/c6sc02464e>
- Rajagopal, K; Maheswari, S; Kathiravan, G (2012) Diversity of endophytic fungi in some tropical medicinal plants – A report. *African Journal of Microbiology Research* **6**(12):2822–2827
<https://doi.org/10.5897/AJMR11.163>
- Reen, FJ; Romano, S; Dobson, ADW; O’Gara, F (2015) The sound of silence: activating silent biosynthetic gene clusters in marine microorganisms. *Marine Drugs* **13**(8):4754–4783
<https://doi.org/10.3390/md13084754>
- Riedling, O; Walker, AS; Rokas, A (2024) Predicting fungal secondary metabolite activity from biosynthetic gene cluster data using machine learning. *Microbiology Spectrum* **12**(2):e03400-23
<https://doi.org/10.1128/spectrum.03400-23>
- Roy, S; Saha, S; Mondal, A (2025) Predicting interactions among species in ecological networks: a roadmap to address Eltonian shortfall. In: Ghosh, L; De, A (Eds.) *Artificial Intelligence and Animal Ecology: A Review* (1st ed.). CRC Press
<https://doi.org/10.1201/9781003492788>
- Sagita, R; Quax, WJ; Haslinger, K (2021) Current state and future directions of genetics and genomics of endophytic fungi for bioprospecting efforts. *Frontiers in Bioengineering and Biotechnology* **9**:649906
<https://doi.org/10.3389/fbioe.2021.649906>
- Shankar, A; Sharma, KK (2022) Fungal secondary metabolites in food and pharmaceuticals in the era of multi-omics. *Applied Microbiology and Biotechnology* **106**(9):3465–3488
<https://doi.org/10.1007/s00253-022-11945-8>
- Sharma, SK; Singh, SK; Ramesh, A; Sharma, PK; Varma, A; Ahmad, E; Khande, R; Singh, UB; Saxena, AK (2018) Microbial genetic resources: status, conservation, and access and benefit-sharing regulations. In: Sharma, S; Varma, A (Eds.). *Microbial Resource Conservation. Soil Biology* **54**. Springer, Cham.
https://doi.org/10.1007/978-3-319-96971-8_1
- Shishodia, SK; Thakur, R; Shankar, J; Singh, R; De Los Rios-Escalante, P (2025) Unlocking endophytic mysteries by leveraging multi-omics technologies. In: Meena, M; Zehra, A; Swapnil, P (Eds.) *Multi-omics Approach to Investigate Endophyte Diversity* **53**:125–144. Springer, Singapore
https://doi.org/10.1007/978-981-96-4100-0_6
- Shu, H; Chen, X; Jiang, Q; Wang, Y; Wan, Z; Xu, J; Wang, P (2024) Optimization of fungal secondary metabolites production via response surface methodology coupled with multi-parameter optimized artificial neural network model. *Bioresource Technology* **413**:131495
<https://doi.org/10.1016/j.biortech.2024.131495>
- Tella, A; Jatto, EO; Ajani, YA (2025) Preserving indigenous knowledge: Leveraging digital technology and artificial intelligence. *IFLA Journal* **51**(3):703–721
<https://doi.org/10.1177/03400352251342505>
- Theobald, S; Vesth, TC; Rendsvig, JK; Nielsen, KF; Riley, R; de Abreu, LM; Salamov, A; Frisvad, JC; Larsen, TO; Andersen, MR; Hoof, JB (2018) Uncovering secondary metabolite evolution and biosynthesis using gene cluster networks and genetic dereplication. *Scientific Reports* **8**(1), 17957
<https://doi.org/10.1038/s41598-018-36561-3>
- Tiwari, P; Adil, M; Park, KI (2025) Biopriming with endophytes improves plant resilience to develop climate-smart, futuristic agricultural crops. *World Journal of Microbiology and Biotechnology* **41**(8), 272
<https://doi.org/10.1007/s11274-025-04485-6>
- Tiwari, P; Bae, H (2022) Endophytic fungi: key insights, emerging prospects, and challenges in natural product drug discovery. *Microorganisms* **10**(2), 360
<https://doi.org/10.3390/microorganisms10020360>

- Tomm, HA; Ucciferri, L; Ross, AC (2019) Advances in microbial culturing conditions to activate silent biosynthetic gene clusters for novel metabolite production. *Journal of Industrial Microbiology and Biotechnology* **46**(9-10):1381–1400
<https://doi.org/10.1007/s10295-019-02198-y>
- Varghese, S; Jisha, MS; Rajeshkumar, KC; Gajbhiye, V; Alrefaei, AF; Jeewon, R (2024) Endophytic fungi: a future prospect for breast cancer therapeutics and drug development. *Heliyon* **10**(13):e33995
<https://doi.org/10.1016/j.heliyon.2024.e33995>
- Varghese, S; Rajeshkumar, KC; Jisha, MS (2025). Discovering the chemotherapeutic potential of bioactive compounds synthesized by endophytic fungi from medicinal plants. In: Meshram, V; Shukla, KK; Gupta, M; Akhtar, N. (Eds.). *Natural Bioactives from the Endophytes of Medicinal Plants (1st ed.)*. CRC Press.
<https://doi.org/10.1201/9781003486275>
- Verma, A; Tiwari, H; Singh, S; Gupta, P; Rai, N; Singh, SK; Singh, BP; Rao, S; Gautam, V (2023) Epigenetic manipulation for secondary metabolite activation in endophytic fungi: current progress and future directions. *Mycology* **14**(4):275–291
<https://doi.org/10.1080/21501203.2023.2241486>
- Wang, Y; Mao, X-M (2025) Mining silent biosynthetic gene clusters for natural products in filamentous fungi. *Chemistry & Biodiversity* **22**:e202402715
<https://doi.org/10.1002/cbdv.202402715>
- Wang, Y; Luo, X; Zou, Q (2022) Effector-GAN: prediction of fungal effector proteins based on pretrained deep representation learning methods and generative adversarial networks. *Bioinformatics* **38**(14):3541–3548
<https://doi.org/10.1093/bioinformatics/btac374>
- Wang, Z; Yu, J; Wang, C; Hua, Y; Wang, H; Chen, J (2025) The deep mining era: genomic, metabolomic, and integrative approaches to microbial natural products from 2018 to 2024. *Marine Drugs* **23**(7), 261
<https://doi.org/10.3390/md23070261>
- Wen, J; Okyere, SK; Wang, S; Wang, J; Xie, L; Ran, Y; Hu, Y (2022) Endophytic fungi: an effective alternative source of plant-derived bioactive compounds for pharmacological studies. *Journal of Fungi* **8**(2), 205
<https://doi.org/10.3390/jof8020205>
- Yang, Y; Liu, X; Cai, J; Chen, Y; Li, B; Guo, Z; Huang, G (2019) Genomic characteristics and comparative genomics analysis of the endophytic fungus *Sarocladium brachiariae*. *BMC Genomics* **20**(1), 782
<https://doi.org/10.1186/s12864-019-6095-1>
- Yu, H; Wang, C; Xue, M (2024) Improved XLNet modeling for Chinese named entity recognition of edible fungus. *Frontiers in Plant Science* **15**:1368847
<https://doi.org/10.3389/fpls.2024.1368847>
- Yuan, J; Zhang, W; Sun, K; Tang, MJ; Chen, PX; Li, X; Dai, CC (2019) Comparative transcriptomics and proteomics of *Atractylodes lancea* in response to endophytic fungus *Gilmaniella* sp. AL12 reveals regulation in plant metabolism. *Frontiers in Microbiology* **10**:1208
<https://doi.org/10.3389/fmicb.2019.01208>
- Yuan, Y; Shi, C; Zhao, H (2023) Machine Learning-enabled genome mining and bioactivity prediction of natural products. *ACS Synthetic Biology* **12**(9):2650–2662
<https://doi.org/10.1021/acssynbio.3c00234>
- Zakariyah, RF; Ajijolakewu, KA; Ayodele, AJ; Folami-A, BI; Samuel, EP; Otuoze, SO; Abdulrauf, LB; Ahmed, RN (2024) Progress in endophytic fungi secondary metabolites: biosynthetic gene cluster reactivation and advances in metabolomics. *Bulletin of the National Research Centre* **48**(1), 44
<https://doi.org/10.1186/s42269-024-01199-x>
- Zhang, J; Lu, J; Zhu, Y; Shen, X; Zhu, B; Qin, L (2024) Roles of endophytic fungi in medicinal plant abiotic stress response and TCM quality development. *Chinese Herbal Medicines* **16**(2):204–213
<https://doi.org/10.1016/j.chmed.2023.02.006>

- Zhao, S; Yin, R; Zhang, M; Zhai, Z; Shen, Z; Mou, Y; Xu, D; Zhou, L; Lai, D (2024) Efficient gene editing in the slow-growing, non-sporulating, melanized, endophytic fungus *Berkleasmium* sp. Dzf12 using a CRISPR/Cas9 system. *World Journal of Microbiology and Biotechnology* **40**(6), 176
<https://doi.org/10.1007/s11274-024-03988-y>
- Zhou, Y; Liu, D; Huang, Z; Xie, X; Lin, W; Zhang, L; Fan, A; Liu, Z (2025) f-BGM enables fungi-specific genome mining in high accuracy and interpretability. *bioRxiv (Preprint)*
<https://doi.org/10.1101/2025.07.08.662937>

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Spore dextrinoidity in the genus *Cortinarius* s.l.

(Versione italiana a pag. 30)

Marco Raumi

Via D. Popogna 417, I-57128 Livorno, Italy; raumiumberto@libero.it

Key words:

Agaricales
Agaricomycetes
Cortinariaceae
dextrinoid reaction
Melzer's reagent
micrographs
spores
taxonomy

Abstract: An extensive study on the variability of spore dextrinoidity in the genus *Cortinarius* s.l. is proposed. Based on the analysis of a large number of species, carried out both on spore deposits and individual spores mounted on slides, evidence emerges that this character may contribute to the set of parameters used for morphological delimitation of species within *Cortinarius* s.l. Images at 1000× magnification document the range of hues of spore dextrinoidity observed in 54 of the many species analysed. Further contributions will extend the study of spore dextrinoidity to additional species.

INTRODUCTION

Within mycological study, one commonly used parameter is the verification of the presence, in fungal tissues examined (for example, the spore wall and ornamentations, hyphae, basidia and asci), of substances capable of reacting chemically with the Melzer's reagent, producing variations within the blue spectrum (for example, purplish blue, blackish blue or greenish blue). This reaction is considered positive and is referred to as being amyloid. Well-known examples include the amyloid spore wall of some species of the genus *Amanita* Pers. (very useful in mycotoxicology for recognising lethal intoxications from fungi on ingested material), as well as the amyloidy of spore ornamentation in the genera *Russula* Pers., *Lactarius* Pers. and *Melanoleuca* Pat.

On the other hand, when the reaction produces a colour within the natural range of the reagent itself, which ranges from yellow when diluted, such as on slide, to reddish-brown when observed in bulk, such as in the container vial, it is considered negative and called dextrinoid reaction. In both cases, the reaction outcome can contribute to the morphological definition of a fungal species.

Furthermore, in some cases, dextrinoidity is used intensively in the taxonomy of an entire genus and not only applied to individual species. The clearest example of this extensive use is found in the genus *Hebeloma* (Fr.) P. Kumm. (Grilli *et al.* 2016), to which may be added the recent proposal by Miller, Ostuni, Angelini & Voto (2025) to also apply it to the genus *Pseudobaeospora* Singer. This method is due to the fact that the dextrinoid reaction can be very variable ranging from no or very weak tones, in the yellow range, to very saturated tones, in the red-brown range.

Some authors, for example Liimatainen *et al.* (2022), treat the genus *Cortinarius* s.l. as divided into several genera, the principal ones being *Calonarius* Niskanen & Liimat., *Cortinarius* (Pers.) Gray s. str. [including the genera *Cortinarius*, *Dermocybe* (Fr.) Wünsche, *Hydrocybe* (Fr. ex Rabenh.) Wünsche, *Myxaciium* (Fr.) P. Kumm., *Rozites* P. Karst., *Sericeocybe* Rob. Henry and *Telamonia* (Fr.) Wünsche], and *Phlegmacium* (Fr.) Wünsche. To date, no specific studies appear to have addressed the variability of the dextrinoid reaction in the genus *Cortinarius* s.l., nor its potential as a differential taxonomic element among species. In the present contribution, based on the examination of numerous species of *Cortinarius* s.l., it is shown that Melzer's reagent produces a highly variable chromatic response spanning a wide range of hues. This reaction has also the advantage of occurring immediately upon contact and remaining stable over time.

Finally, it is useful to note that in species of *Cortinarius* s.l., although the spore deposit falls within the rusty-red colour range (Fig. 1), spores observed in water at 1000× magnification generally appear within the greyish green colour range (Fig. 2, next page). This shade therefore provides good contrast with the various nuances of the dextrinoid reaction. In contrast, based on our numerous observations, staining with Congo red typically reveals a greenish coloration in the spore body and a red-orange tint at the periphery (Fig. 2, next page).

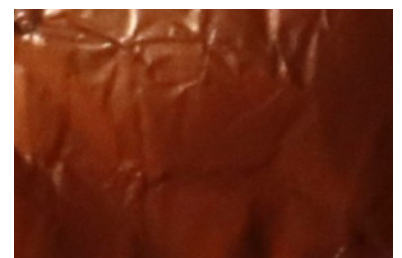


Fig. 1. *C. variegatuloides*

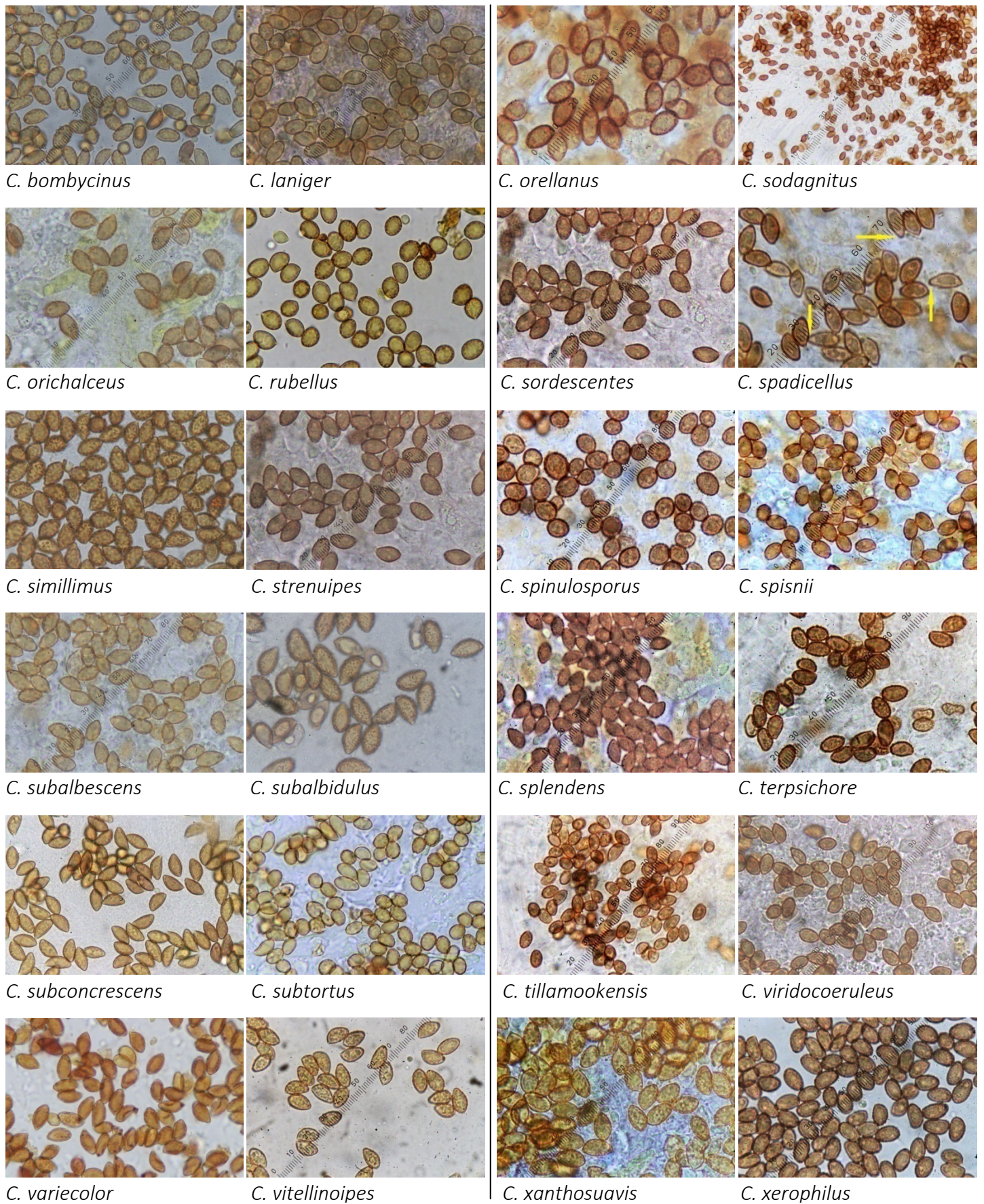


Fig. 2. Spores at 1000× magnification. In the two columns left: in water; in the two columns right: in Congo red

MATERIALS AND METHODS

Microscopic investigation

Melzer's reagent does not require any particular specifications; it is sufficient that it is not out-of-date and

that it is contained in the vials sold by specialised distributors.

For the assessment of dextrinoidity on spore deposits, the spore deposit is transferred, or collected directly, onto a slide. The spore deposit is moistened with small drops of Melzer's reagent which is then delicately washed out with small drops of chloral hydrate, taking care not to cause the dispersion of the spores on the surface of the slide; finally the prepared slide is covered with a coverslip. Alternatively, the spore deposit can be collected on a strip of transparent adhesive tape which, after the application of the two aforementioned reagents, is inverted and fixed onto the slide (in this case the application of the coverslip is no longer necessary). This procedure helps limit spore dispersion during the application of the two mounting media. The preparation is then observed and photographed.

Following numerous tests, it was found that the colour tone perceived at low magnifications (for example, 100×) appears in most cases darker than when the same spore deposit is observed at 1000× magnifications. In this contribution all observations were carried out at 1000× magnification.

When spores are observed on lamellar fragments, they are found at different stages of maturation, resulting in variable chromatic reactions to the Melzer's reagent (Fig. 3). In order to maximize the presence of mature spores, and thus the correct chromatic definition of the dextrinoid reaction, in this contribution the observations were always carried out on spore deposit.

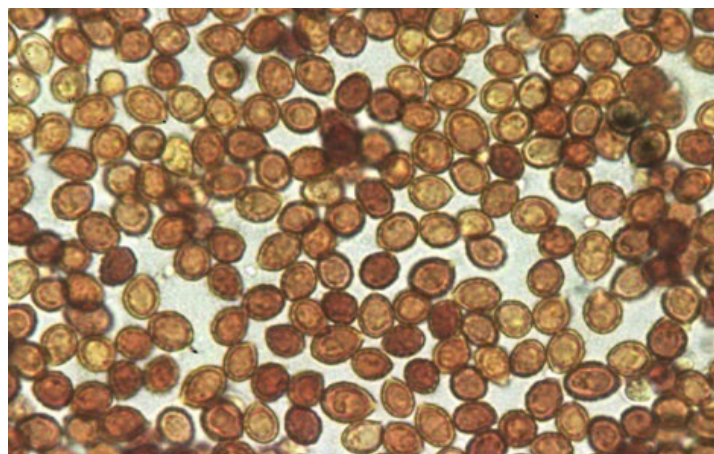


Fig. 3. *C. cotoneus*

In some species, the dextrinoid reaction is not uniform but shows two different pigments, which may be distributed in patches or separated between the central body and the periphery of the spore. In other cases the central guttula may take on a different colour from the rest of the spore. In all these situations, it is difficult to select a single colour that is representative of the dextrinoid reaction of that species; the procedure adopted here is therefore to simply note these occurrences without proposing a colour code (Figs. 4 and 5).

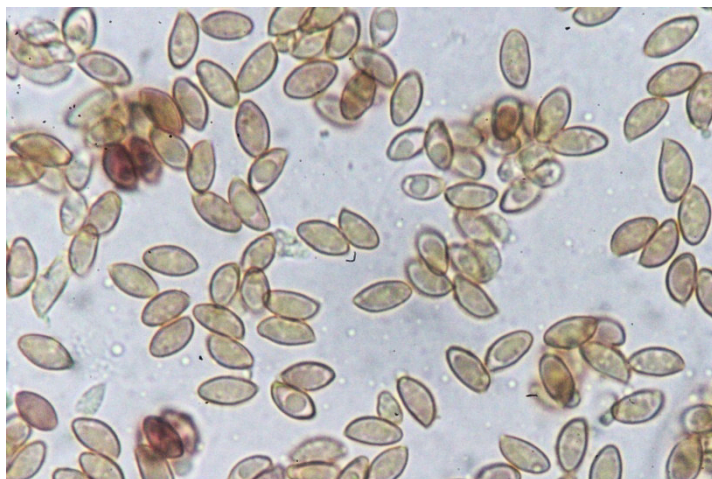


Fig. 4. *C. turmalis*

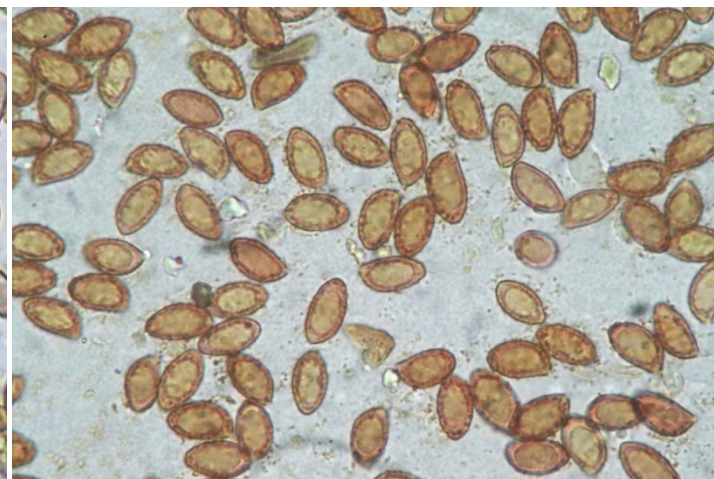


Fig. 5. *C. tremulinus*

In several species of *Cortinarius* s.l. (for example, some of the genus *Phlegmacium*) the spores have a papillate germinating apex and this, upon contact with Melzer's reagent, often turns yellow. This localised reaction is here excluded from the chromatic definition of dextrinoidity.

Micrographic documentation tools

Microscope

Microscopes, like any other optical instrument, are equipped with a light source. This is essentially of two

types: a halogen lamp or one or more LED sources. The halogen lamp provides light with a colour temperature of approximately 3000 K, meaning that its emission spectrum enhances warm colours such as yellow and orange. In contrast, the LED source can be supplied with different colour temperatures; it should be noted that higher values, for example around 5000–6000 K, tend to enhance colours such as green and blue. Nevertheless, under the optical conditions of the microscopic observations discussed here, these variations have only a minimal effect on the perceived colours.

It should also be noted that different optical microscopes may not yield identical colour rendering. However, in the rare cases in which the same collection was examined with different microscopes, the results were consistent or showed only negligible differences.

For this study, a Nikon Eclipse E 200 microscope equipped with a halogen light source with a colour temperature of 3000 K was used.

Photographic reproduction

In micrography, the imaging device used is also a relevant factor; the colour captured in an image may vary depending on the type (smartphone, digital camera, video camera), as well as its quality and calibration. The use of high-quality equipment with adequate resolution is therefore recommended.

When using a digital camera, it can be operated either in manual mode or in automatic mode. In manual mode, all parameters are set by the operator and kept constant for each photo, ensuring a consistent photographic product. In automatic mode, the camera adjusts parameters independently for each shot; this may result in slight colour differences between images due to variations in settings such as white balance. However, these changes in settings always produce minimal, imperceptible differences (for example, slightly lighter or darker tones) and do not significantly alter the basic colour of the observed spores.

For this study, a Canon EOS R 100 digital reflex camera set in automatic mode was used.

Definition of the observed colours

Given the wide range of colour variations observed in this study, the use of simplified colour code system, such as 'red', 'red-pink', 'red-orange', 'purple', 'green', 'light green' etc., was clearly ineffective. It was therefore necessary to assign numerical reference codes to the observed colour tones, linked to a standardised colour chart. Among the various systems available, the NCS S system (where “S” denotes the second standardised edition) was selected.

The NCS colour system is widely adopted internationally for standardised colour communication. This system was developed in the last century by NCS color AB of Stockholm and the acronym stands for Natural Color System. It represents a logical system of colours based on the way they are perceived by the naked eye (physiological and physical chemistry of the human visual system). The NCS system is internationally recognised as a universal language of colour.

The NCS S coding system is entirely based on human perception of colours and not on their mixing. Its official colour atlas comprises 1950 distinct colour samples.

The NCS S colour atlas can be obtained in physical form (e.g. colour fan decks) from paint retailers or industrial suppliers. Alternatively, several online resources reproduce the full set of 1950 NCS S colours. In the present study, this second approach was adopted, using the website <https://get-color.com/>.

THE METHOD'S EFFECTIVENESS

Since any comparative colour chart provides a relatively limited set of colours, it is generally difficult to find a 100% exact correspondence between a given colour code, together with its representative colour image, and the colour observed under the microscope. Therefore the chromatic images and the respective codes proposed in this work must necessarily be understood as general indications, with possible, albeit minimal, chromatic deviations compared to the precise colour value actually observed.

In order to allow direct comparison, for each species documented below both the image of the selected NCS S colour code and a micrograph of the spores in water at 1000× magnification are presented.

CONCLUSIONS

In the genus *Cortinarius* s.l., there are relatively few microscopic characters available for species delimitation. The few available concern the variability of spore morphology (subspherical, ellipsoidal, fusiform, amygdaliform, citriform) and ornamentation (from finely to coarsely verrucose); the presence, along the lamellar edge of many species, of sterile terminal elements that are only rarely well differentiated into true cheilocystidia; a rare structuring of the pileipellis in bundles of hyphae simulating a trichoderm instead of the usual cutis or ixocutis; and the rare absence of clamp connections found only in a small group of *Myxacium* (La Chiusa & Papetti 2021). Conversely, some macrochemical reactions (with KOH or NaOH, Lugol or Melzer's reagent) are applied to the surfaces and context of the basidiomes (La Chiusa & Papetti 2021). Among chemically based macroscopic characters, the presence of anthraquinone pigments in *Dermocybe* represent a notable example (Huymann *et al.* 2024).

Given the broad range of colour variation observed, the reaction of the spores to Melzer's reagent can be usefully incorporated as an additional differential micromorphological character, which is also straightforward to assess.

Cortinarius s.l. comprises many taxa worldwide: in Europe alone, more than 2000 species have been described (J.E.C. website). Given its complexity, it is inevitable that pairs or groups of species, often within taxonomic units called stirpes, remain difficult to distinguish, despite the use of morphoanatomical characters, macrochemical reactions, ecological data and phylogenetic analyses. Depending on differing taxonomic interpretations, such taxa may be treated either as distinct species or as synonyms. The same J.E.C. website suggests that the number of acceptable species is less than 2000, probably around 500. It is therefore hoped that the chromatic response of the spores to Melzer's reagent may provide an additional line of evidence to help resolve these taxonomic uncertainties.

Finally, it would be desirable to assess the dextrinoid reaction of a species across multiple samples from different geographic areas. Unfortunately, many species are considered objectively rare, making it difficult to carry out a diversified sampling. As a result, their morphological variability, including spore dextrinoidity, may still be incompletely understood. However, in those species for which sufficiently broad sampling was available, the colour of the dextrinoid reaction proved to be consistent.

REFERENCES

- Grilli, E; Beker, HJ; Eberhardt, U; Schütz, N; Leonardi, M; Vizzini, A (2016) Unexpected species diversity and contrasting evolutionary hypotheses in *Hebeloma* (Agaricales) sections *Sinapizantia* and *Velutipes* in Europe. *Mycol Progress* 15:5
<https://dx.doi.org/10.1007/s11557-015-1148-6>
- Huymann, LR; Hannecker, A; Turrini, G; Liimatainen, K; Niskanen, T; Probst, M; Peintner, U; Siewert, B (2024) Revised taxon definition in European *Cortinarius* subgenus *Dermocybe* based on phylogeny, chemotaxonomy, and morphology. *Mycol Progress* 23:26
<https://doi.org/10.1007/s11557-024-01959-z>
- J.E.C. website, <https://www.jec-cortinarius.org/English/genre.html> (accessed April 18, 2026)
- La Chiusa, L.; Papetti, C (2021) Approccio al Genere *Cortinarius* con chiavi dicotomiche per la determinazione di Sottogeneri, Sezioni e specie. prima parte. *Bollettino C.M. "G. Carini"* 82:1–47
- Liimatainen, K; Kim, JT; Pokorny, L; Kirk, PM; Dentinger, B; Niskanen, T (2022) Taming the beast: a revised classification of *Cortinariaceae* based on genomic data. *Fungal Diversity* 112:89–170
<https://doi.org/10.1007/s13225-022-00499-9>
- Miller, K; Ostuni, S; Angelini, C; Voto, P (2025) Studies in *Pseudobaeospora* from Puerto Rico and Florida. *MycolObs* 14:32–49

Destrinoidia sporale nel genere *Cortinarius* s.l.

Parole chiave:

Agaricales
Agaricomycetes
Cortinariaceae
 micrografie
 reagente di Melzer
 reazione destrinoide
 spore
 tassonomia

Riassunto: Si propone uno studio estensivo sulla variabilità della destrinoidia sporale nel genere *Cortinarius* s.l. Sulla base dell'analisi di un ampio numero di specie, condotta sia su sporata sia su singole spore montate su vetrino, emergono evidenze che questo carattere possa contribuire all'insieme dei parametri usati per la delimitazione morfologica delle specie di *Cortinarius* s.l. Immagini a ingrandimento 1000× documentano i vari cromatismi della destrinoidia sporale riscontrati in 54 delle numerose specie analizzate. Successivi contributi estenderanno lo studio della destrinoidia sporale ad altre specie.

INTRODUZIONE

Nel quadro dello studio della micologia, un parametro comunemente usato è la verifica della presenza, nei tessuti fungini esaminati (ad es., la parete e le ornamentazioni sporali, ife, basidi e aschi), di sostanze capaci di reagire chimicamente al reagente di Melzer, colorandosi di tonalità nello spettro del blu (ad es. blu-violetto, blu-nerastro, blu-verdastro). Questa reazione è considerata positiva ed è definita amiloide. È ben nota, ad esempio, l'amiloidia della parete sporale di alcune specie del genere *Amanita* Pers. (molto utile in micotossicologia per il riconoscimento su materiale ingerito di intossicazioni letali da funghi), così come quella delle ornamentazioni sporali nei generi *Russula* Pers., *Lactarius* Pers. e *Melanoleuca* Pat. Quando, viceversa, la reazione produce una colorazione nella gamma del colore naturale del reagente, che spazia dal giallo quando è osservato diluito, come sul vetrino, al bruno-rossastro quando è osservato in massa, come nella boccetta contenitore, essa viene considerata negativa e si parla di reazione destrinoide. In entrambi i casi, l'esito della reazione può contribuire alla definizione morfologica di una specie fungina.

In alcuni casi, inoltre, la destrinoidia viene usata in modo intensivo nella tassonomia di un intero genere e non solo applicata a singole specie. L'esempio più evidente di questo suo utilizzo esteso si riscontra nel genere *Hebeloma* (Fr.) P. Kumm. (Grilli *et al.* 2016), cui si aggiunge la recente proposta di Miller, Ostuni, Angelini & Voto (2025) di applicarla anche al genere *Pseudobaeospora* Singer. Questo metodo è dovuto al fatto che la reazione destrinoide può essere molto variabile spaziando da nulla o toni molto deboli, nella gamma del giallo, a toni molto saturi, nella gamma del rosso-bruno.

Alcuni autori, per esempio Liimatainen *et al.* 2022), trattano il genere *Cortinarius* s.l. come suddiviso in diversi generi, i principali dei quali sono *Calonarius* Niskanen & Liimat., *Cortinarius* (Pers.) Gray s. str. (inclusivo dei generi *Cortinarius*, *Dermocybe* (Fr.) Wünsche, *Hydrocybe* (Fr. ex Rabenh.) Wünsche, *Myxaciium* (Fr.) P. Kumm., *Rozites* P. Karst., *Sericeocybe* Rob. Henry e *Telamonia* (Fr.) Wünsche], e *Phlegmacium* (Fr.) Wünsche. Ad oggi, non risultano studi specifici sulla variabilità della reazione destrinoide nel genere *Cortinarius* s.l., né sul suo potenziale utilizzo come carattere tassonomico differenziale tra le specie. Nel presente contributo si mostra, sulla base di numerose specie di *Cortinarius* s.l. testate, che il reagente di Melzer produce una reazione cromatica altamente variabile che spazia su un'ampia gamma di toni. Tale reazione presenta anche il vantaggio di manifestarsi immediatamente al contatto e di mantenersi stabile nel tempo.

È infine, opportuno notare che nelle specie di *Cortinarius* s.l., sebbene la polvere sporale si collochi nella gamma della tonalità rosso-ruggine (Fig. 1), le spore osservate in acqua a 1000× ingrandimenti appaiono generalmente nella gamma cromatica del verde grigiastro (Fig. 2 pag. seg.). Questa tonalità offre quindi un buon contrasto rispetto alle varie sfumature della reazione destrinoide. A contatto con il rosso Congo, invece, le nostre diverse osservazioni evidenziano generalmente una tonalità verdastra nel corpo sporale e rosso-arancione nella periferia (Fig. 2 pag. seg.).

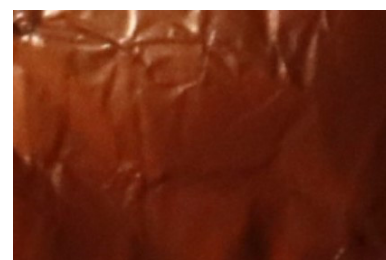


Fig. 1. *C. variegatuloides*

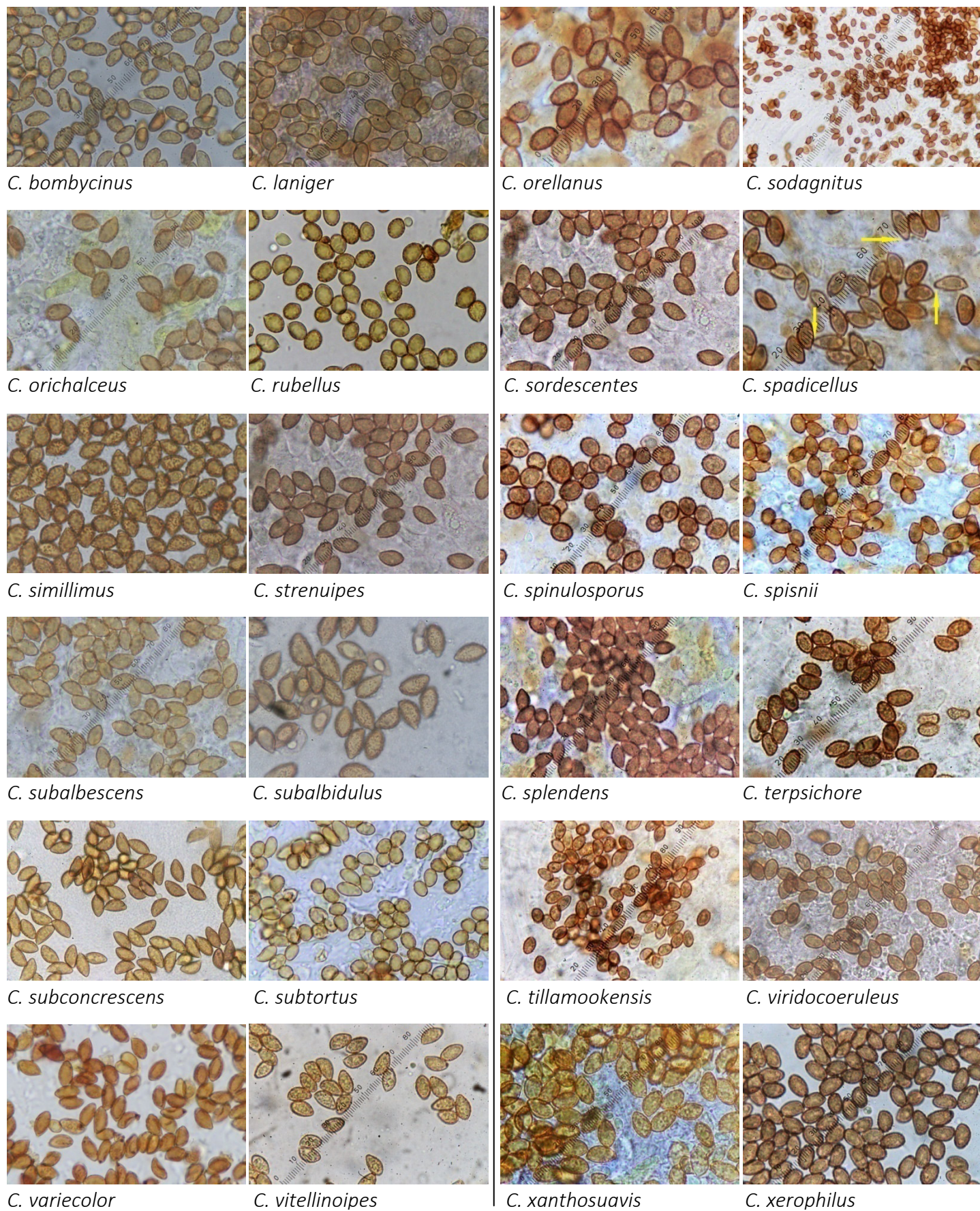


Fig. 2. Spore a ingrandimento 1000x. Le due colonne a sx: in acqua; le due colonne a dx: in rosso Congo

MATERIALI E METODI

Indagine microscopica

Il reattivo di Melzer non richiede specifiche particolari; è sufficiente che non sia scaduto e che sia contenuto nelle boccette vendute dai distributori specializzati.

Per la valutazione della destrinoidia da sporata, il deposito sporale viene trasferito, o raccolto direttamente, su un vetrino portaoggetto. Si bagna il deposito sporale con piccole gocce di reattivo di Melzer che viene poi dilavato delicatamente con piccole gocce di Cloralio idrato, facendo attenzione a non causare la dispersione delle spore sulla superficie del vetrino; infine si copre il preparato con un vetrino coprioggetto. In alternativa, il deposito sporale può essere raccolto su una striscia di nastro adesivo trasparente che, dopo l'applicazione dei due liquidi sopra citati, viene rovesciata e fissata sul vetrino portaoggetti (in questo caso l'applicazione del vetrino coprioggetto non è più necessaria). Questa procedura aiuta a contenere la dispersione delle spore durante l'applicazione dei due mezzi di montaggio. Il preparato viene poi osservato e fotografato.

In seguito a numerose verifiche si è constatato che la tonalità di colore percepita a bassi ingrandimenti (per esempio, 100x) si presenta nella maggior parte dei casi più scura rispetto all'osservazione della stessa sporata a 1000x ingrandimenti. In questo contributo tutte le osservazioni sono state eseguite a 1000x ingrandimenti.

Quando le spore sono osservate su frammenti di lamella, si trovano sempre spore a diversi stadi di maturazione con conseguenti differenti reazioni cromatiche al reattivo di Melzer (Fig. 3). Al fine di massimizzare la presenza di spore mature, e quindi la corretta definizione cromatica della reazione destrinoide, in questo contributo le osservazioni sono state eseguite sempre su sporata.

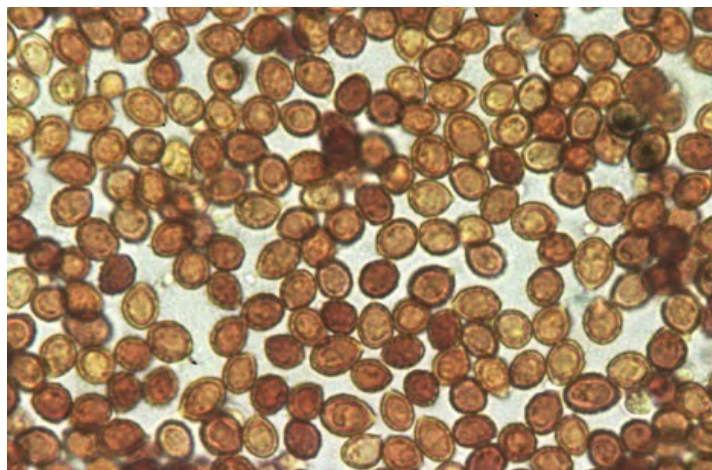


Fig. 3. *C. cotoneus*

In alcune specie, la reazione destrinoide non è uniforme ma mostra due pigmenti diversi che possono essere distribuiti in chiazze oppure separati tra corpo centrale e periferia della spora. In altri casi la guttula centrale può assumere un colore diverso dal resto della spora. In tutte queste situazioni risulta difficile selezionare un unico colore che sia rappresentativo della reazione destrinoide di quella specie; la procedura qui adottata è allora quella di limitarsi a evidenziare tali evenienze senza proporre un codice colore (Fig. 4 e 5).

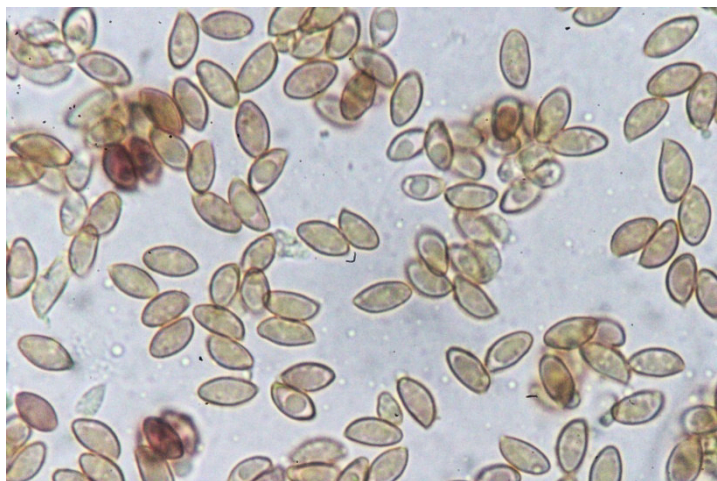


Fig. 4. *C. turmalis*

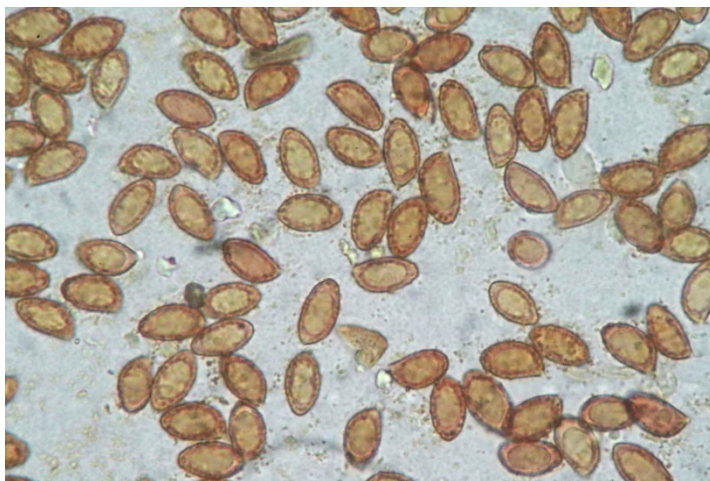


Fig. 5. *C. tremulinus*

In diverse specie di *Cortinarius* s.l. (p. es., alcune del genere *Phlegmacium*) le spore presentano un apice germinativo papillato e questo, al contatto con il reagente del Melzer, sovente si tinge di giallo. Questa reazione localizzata viene qui esclusa dalla definizione cromatica della destrinoidia.

Strumenti per la documentazione micrografica

Microscopio

I microscopi, come qualunque altro strumento ottico, sono forniti di una fonte luminosa. Questa può essere, essenzialmente, di due tipologie: una lampadina alogena oppure uno o più sorgenti luminose a LED. La lampadina alogena fornisce una luce con una temperatura di colore di circa 3000 K, ciò significa che il suo spettro luminoso esalta leggermente di più le colorazioni calde come il giallo e l'arancione. Viceversa, la sorgente luminosa a LED può essere fornita con diverse temperature di colore; in questo caso si dovrà tenere presente che a valori maggiori, per esempio intorno ai 5000–6000 K, tendono ad essere esaltati colori come il verde e l'azzurro. Ciononostante, a livello ottico delle osservazioni al microscopio qui trattate, tali variazioni dei colori percepiti rimangono di una influenza molto minima.

Va inoltre notato che microscopi ottici diversi potrebbero non fornire la stessa resa cromatica. Tuttavia, nei rari casi in cui le osservazioni di una stessa raccolta sono state effettuate con più microscopi diversi, l'esito è risultato costante o solo trascurabilmente differente.

Per questo studio è stato usato un microscopio Nikon Eclipse E 200 con fonte luminosa alogena con una temperatura di colore di 3000 K.

Riproduzione fotografica

Per la micrografia, assume rilevanza anche lo strumento di acquisizione immagini usato; il colore catturato nell'immagine, infatti, può variare in base alla natura (cellulare, fotocamera digitale, videocamera) dello strumento usato, oltre che alla sua taratura e qualità. È pertanto preferibile utilizzare strumenti di alta qualità con ottima risoluzione.

Nel caso di una macchina fotografica digitale, di tipo reflex, essa può essere gestita in modalità manuale o in modalità automatica. Nella modalità manuale, tutti i parametri vengono impostati manualmente dall'operatore e tenuti costanti ad ogni foto; in questo viene garantito un prodotto fotografico coerente. Nella modalità automatica, la fotocamera decide autonomamente come impostare i parametri di volta in volta; in questo modo viene acquisito un prodotto leggermente diverso in colore tra le varie foto scattate a causa di impostazioni non costanti dei parametri, come ad esempio quello del bilanciamento del bianco. Comunque, queste variazioni di impostazioni producono sempre differenze minime, impercettibili (per esempio, toni un po' più chiari o più scuri) che non alterano significativamente il colore di base delle spore osservate.

Per questo studio è stata usata una macchina fotografica digitale reflex Canon EOS R 100 impostata in modalità automatica.

Definizione dei colori osservati

Davanti all'ampio ventaglio di cromatismi riscontrati in questo studio, l'uso di un sistema di codifica cromatica semplificata, del tipo 'rosso', 'rosso-rosa', 'rosso-arancio', 'viola', 'verde', 'verde pallido' ecc., è risultato evidentemente inefficace. Ne è quindi conseguita l'esigenza di dare ai vari cromatismi riscontrati un codice numerico di riferimento che fosse abbinato ad una specifica tabella colore. Fra i tanti disponibili, la scelta è caduta sul sistema NCS S (dove il codice "S" identifica la seconda versione standardizzata).

Il sistema di colore NCS è ampiamente adottato a livello internazionale come comunicazione standardizzata del colore. Questo sistema è stato sviluppato nel secolo scorso da NCS color AB di Stoccolma e l'acronimo sta per Natural Color Sistem (Sistema di Colore Naturale). Esso rappresenta un sistema logico dei colori che si basa sul modo in cui questi sono percepiti dall'occhio nudo (chimica e fisica fisiologica dell'apparato visivo umano). Il sistema NCS è riconosciuto in campo internazionale come linguaggio universale dei colori.

Il sistema di codifica NCS S si basa interamente sulla percezione umana dei colori e non sulla loro mescolanza. Nella sua tabella colore ufficiale sono presenti 1950 campioni di tonalità di colore.

La tabella colore NCS S può essere fisicamente ottenuta (p. es. stecca colore) presso le rivendite di vernici oppure presso le industrie che ne fanno uso. In alternativa, vari siti internet riproducono tutte le 1950 tonalità di colore NCS S. Nel presente studio, è stato adottato questo secondo approccio, usando il sito internet <https://get-color.com/>.

VALIDITÀ DEL METODO

Dal momento che qualsiasi tabella di colore comparativa offre un numero relativamente limitato di colori, risulta generalmente difficile trovare una corrispondenza esatta al 100% tra un dato codice colore, con la relativa immagine cromatica rappresentativa, e il colore osservato al microscopio. Quindi le immagini cromatiche e i rispettivi codici proposti in questo lavoro devono essere necessariamente intesi come indicazioni di massima, con possibili, quantunque minime, deviazioni cromatiche rispetto al preciso valore cromatico effettivamente osservato.

Al fine di consentire un confronto diretto, per ogni specie di seguito documentata vengono presentate sia l'immagine del codice colore NCS S scelto, sia una micrografia in acqua a 1000× ingrandimenti delle spore.

CONCLUSIONI

Nel genere *Cortinarius* s.l., sono disponibili relativamente pochi caratteri microscopici per la delimitazione delle specie. Questi riguardano la variabilità della morfologia (subsferica, ellissoidale, fusiforme, amigdaliforme, citriforme) e dell'ornamentazione (da finemente punteggiata a grossolanamente verrucosa) sporale; la presenza, sul filo lamellare di molte specie, di elementi terminali sterili che peraltro solo raramente sono ben differenziati in veri cheilocistidi; una rara strutturazione della pileipellis in fasci di ife simulanti un tricotoderma invece che in cutis o ixocutis; la rara assenza di giunti a fibbia riscontrata solo in un piccolo gruppo del genere *Myxacium*; (La Chiusa & Papetti 2021). Viceversa, alcune reazioni macrochimiche (con KOH o NaOH, Lugol o reattivo di Melzer) vengono applicate alle superfici e il contesto dei basidiomi (La Chiusa & Papetti 2021). Tra i caratteri macroscopici su base chimica, un importante esempio è rappresentato dalla presenza di pigmenti antrachinonici in *Dermocybe* (vedi, per esempio, Huymann *et al.* 2024).

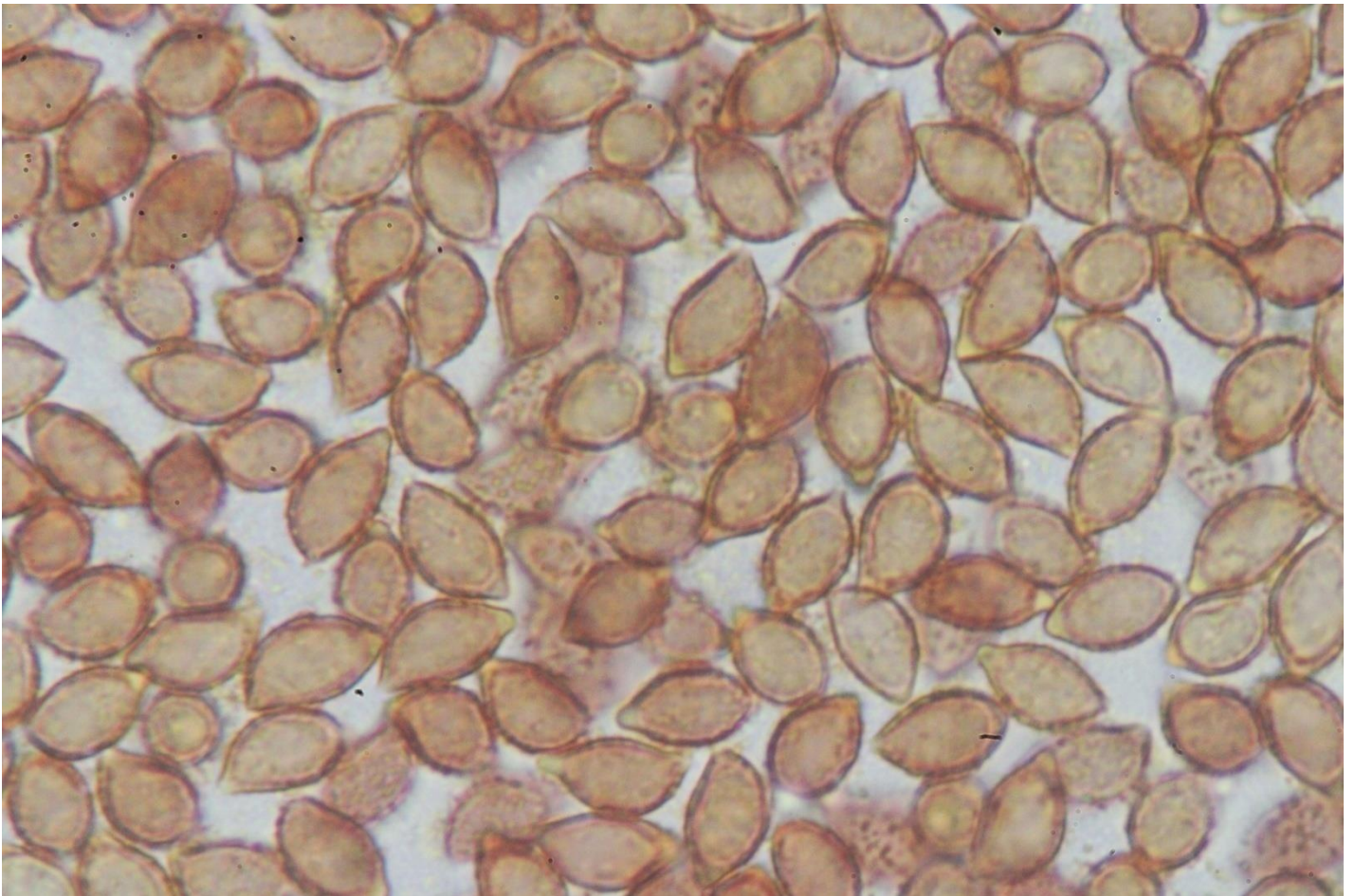
Grazie all'ampia diversificazione dello spettro cromatico osservato, la reazione delle spore al reattivo di Melzer può pertanto essere proficuamente aggiunta come ulteriore carattere micromorfologico differenziale, che è, peraltro, anche di facile osservazione.

Cortinarius s.l. annovera molti taxa nel mondo: nella sola Europa, sono state descritte più di 2000 specie (sito web J.E.C.). Data la sua complessità, è inevitabile che coppie o gruppi di specie, sovente all'interno dei raggruppamenti tassonomici denominati stirpi, risultino difficili da differenziare, malgrado il contributo dell'analisi differenziale basata su caratteri morfoanatomici, reazioni macrochimiche, dati ecologici e analisi filogenetiche. A seconda delle varie interpretazioni tassonomiche, tali taxa potrebbero essere considerati specie distinte o sinonimi. Lo stesso sito web J.E.C. suggerisce che il numero di specie reali sia probabilmente intorno a 500. L'auspicio è che la risposta cromatica delle spore al reattivo di Melzer possa contribuire un elemento investigativo aggiuntivo nella risoluzione di queste criticità tassonomiche.

Come ultima considerazione, sarebbe auspicabile potere annotare la reazione destrinoide di una specie su campioni diversificati provenienti da differenti aree geografiche. Purtroppo, molte specie sono ritenute oggettivamente rare e pertanto è difficile eseguirne una campionatura diversificata. Di conseguenza, la conoscenza della loro variabilità morfologica, che include anche la destrinoidia sporale, potrebbe essere ancora incompleta. Tuttavia, per le specie su cui è stato possibile effettuare una campionatura sufficientemente diversificata, il colore della reazione destrinoide è risultato sempre costante.



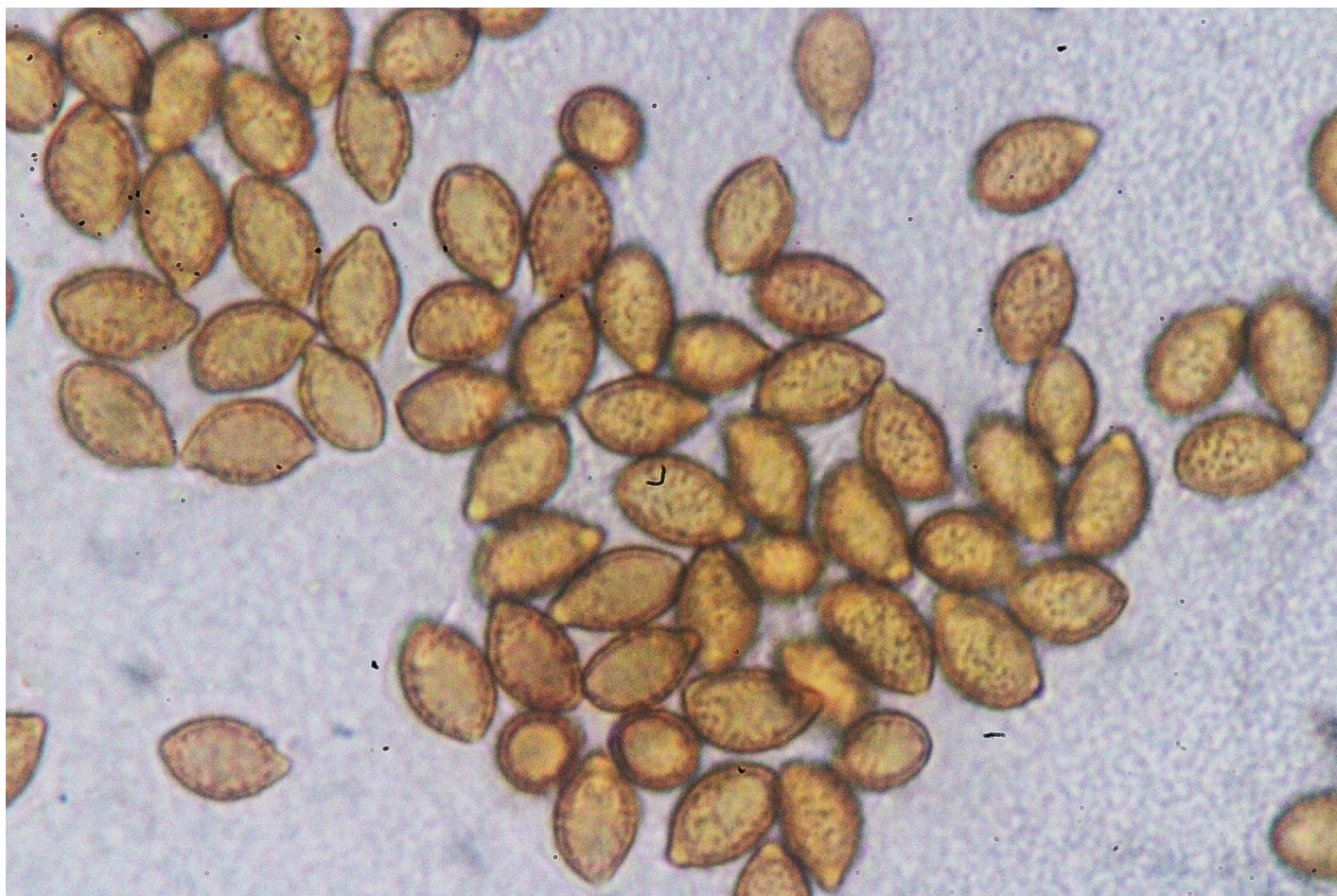
NCS-S 2020-y30r



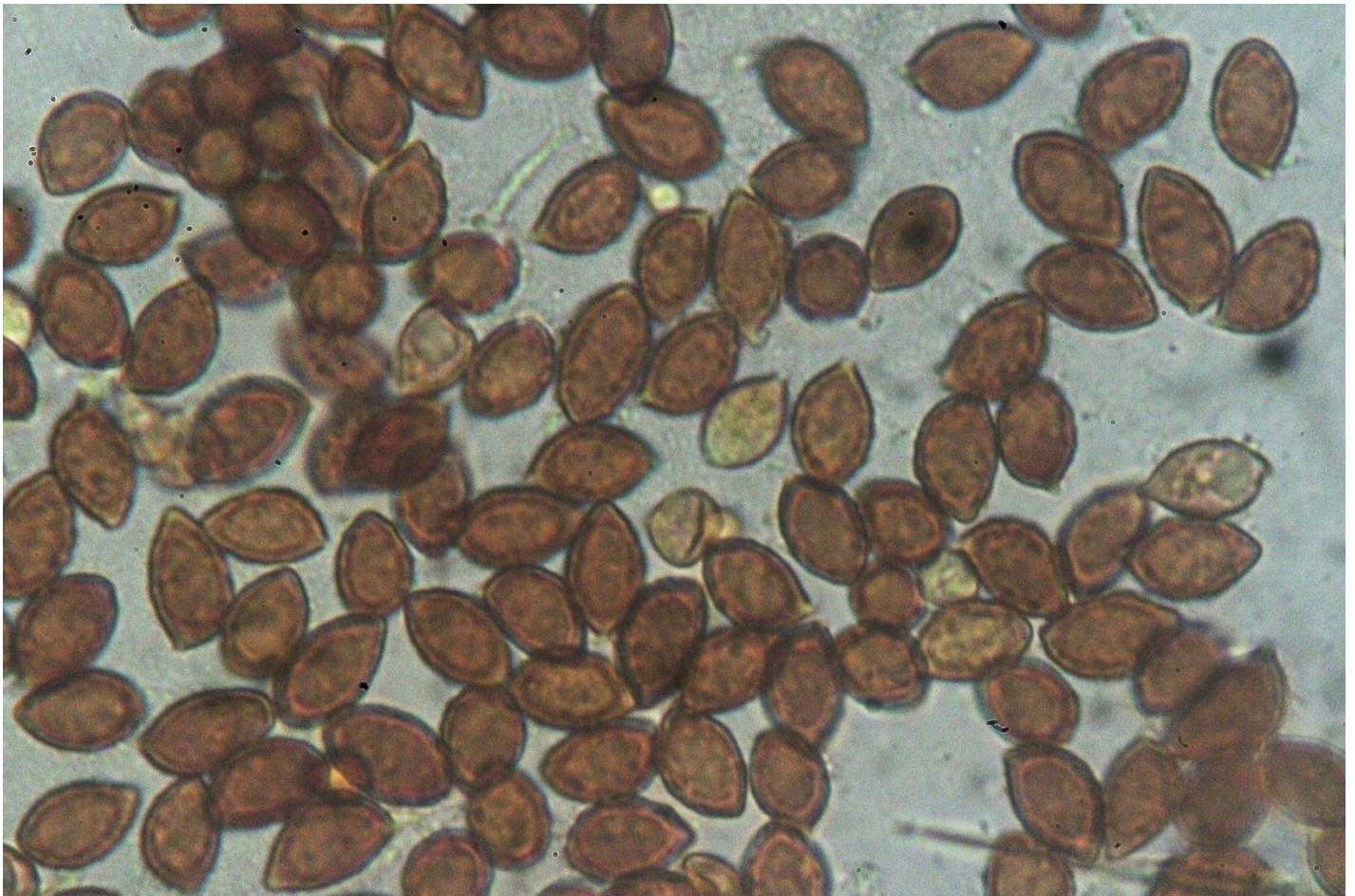
Cortinarius aleuriosmus Maire



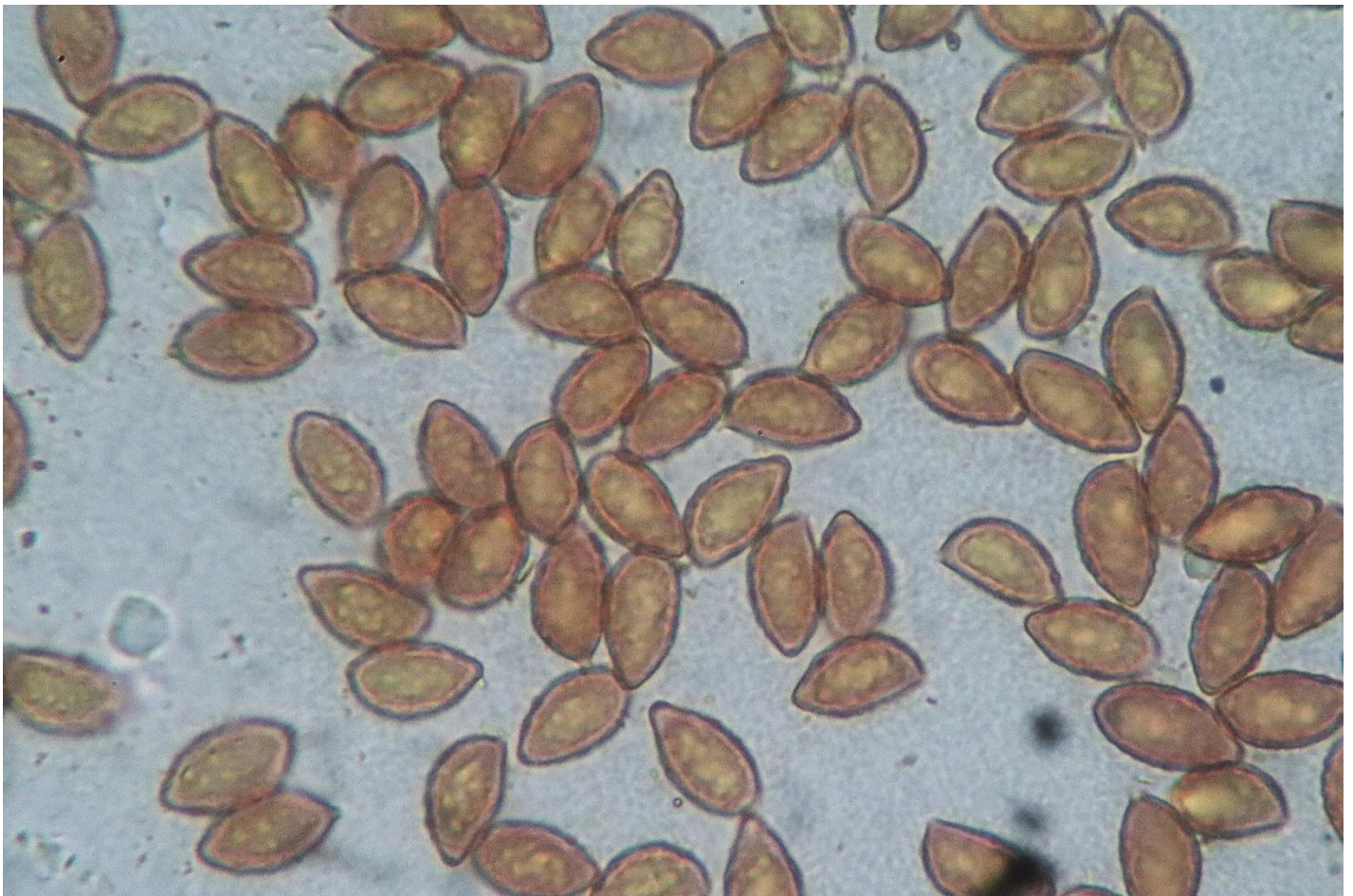
NCS S 2040-y10r



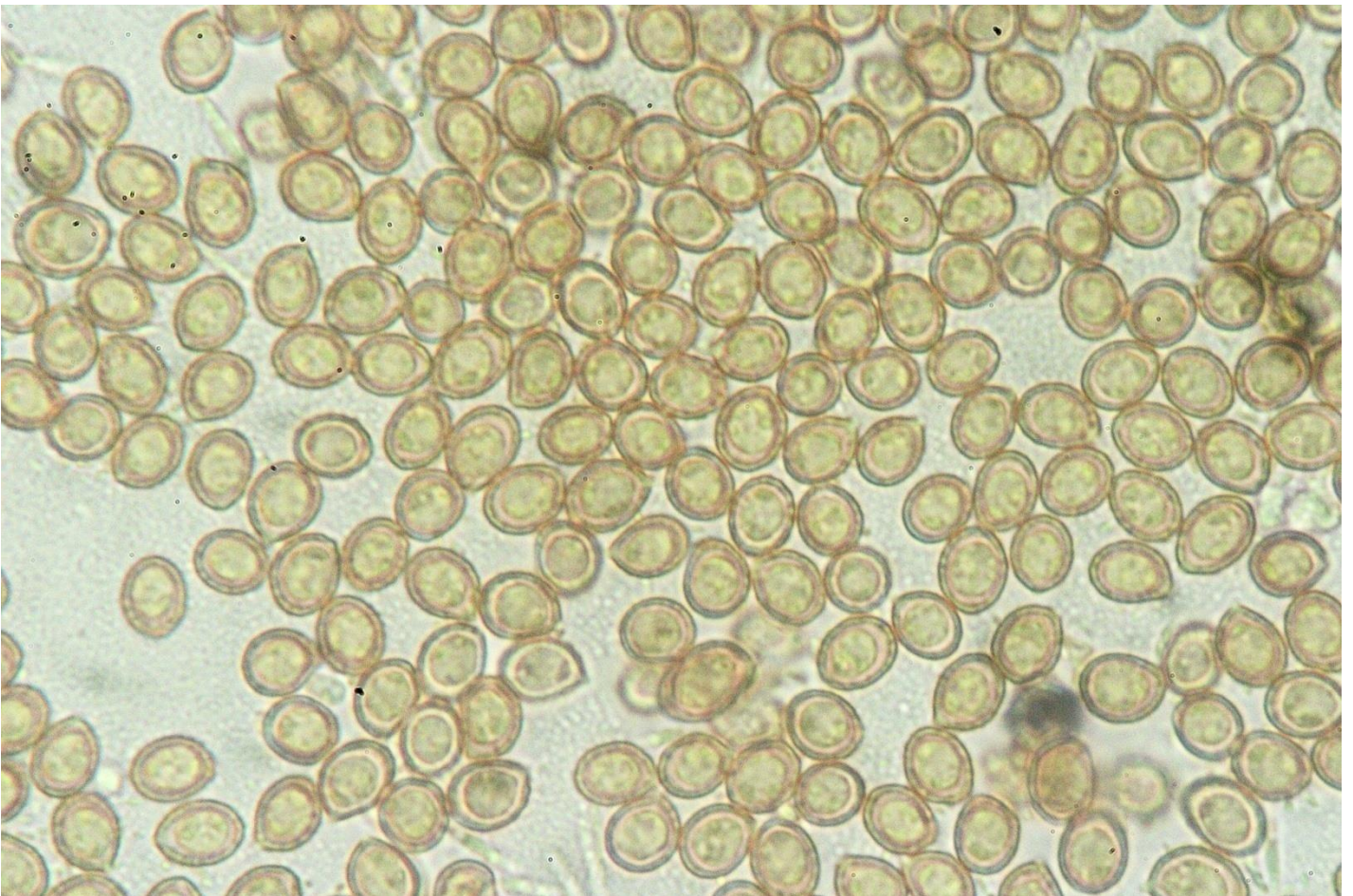
Cortinarius amoenolens Rob. Henry ex P.D. Orton



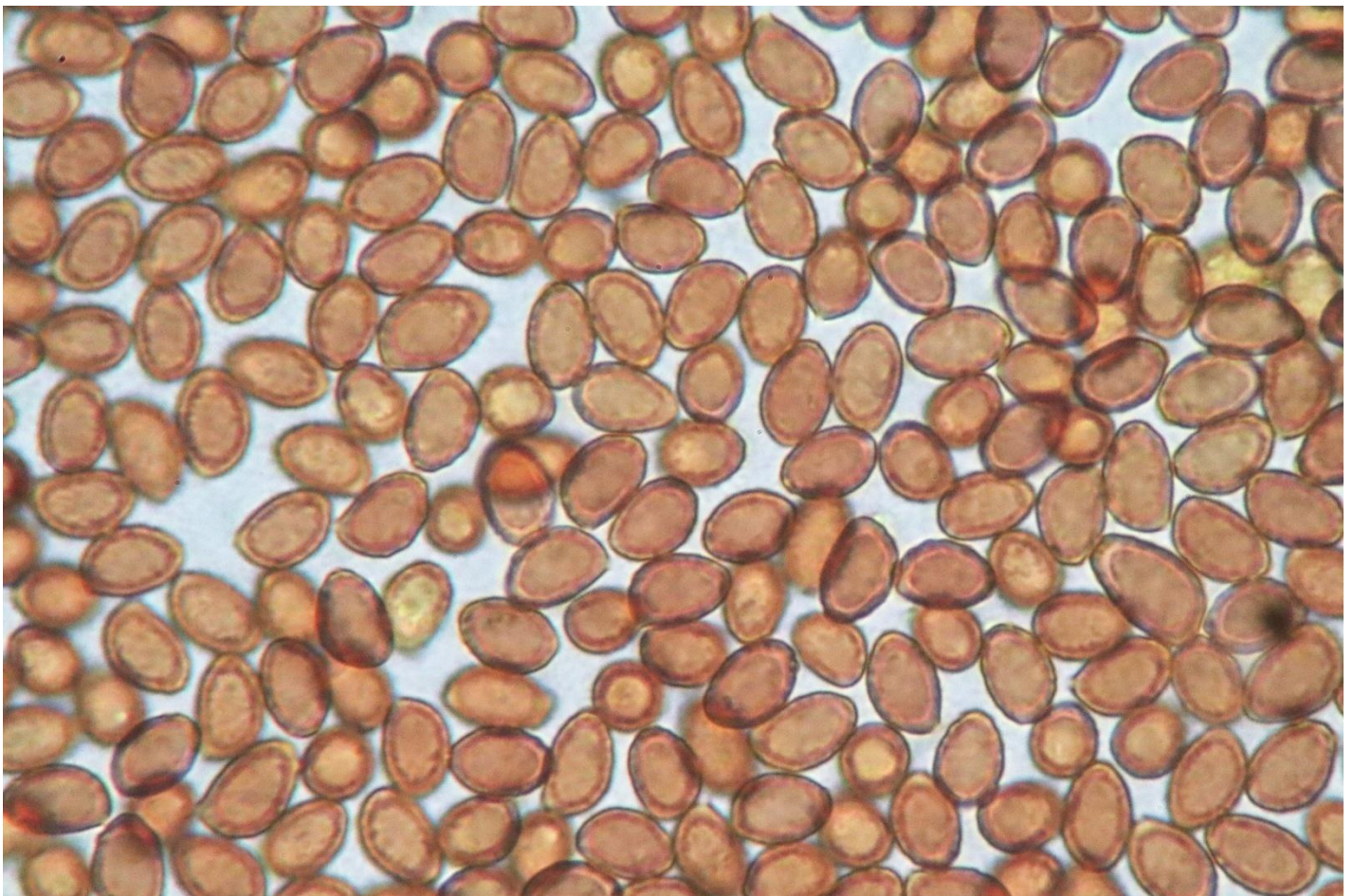
Cortinarius arcuatorum Rob. Henry



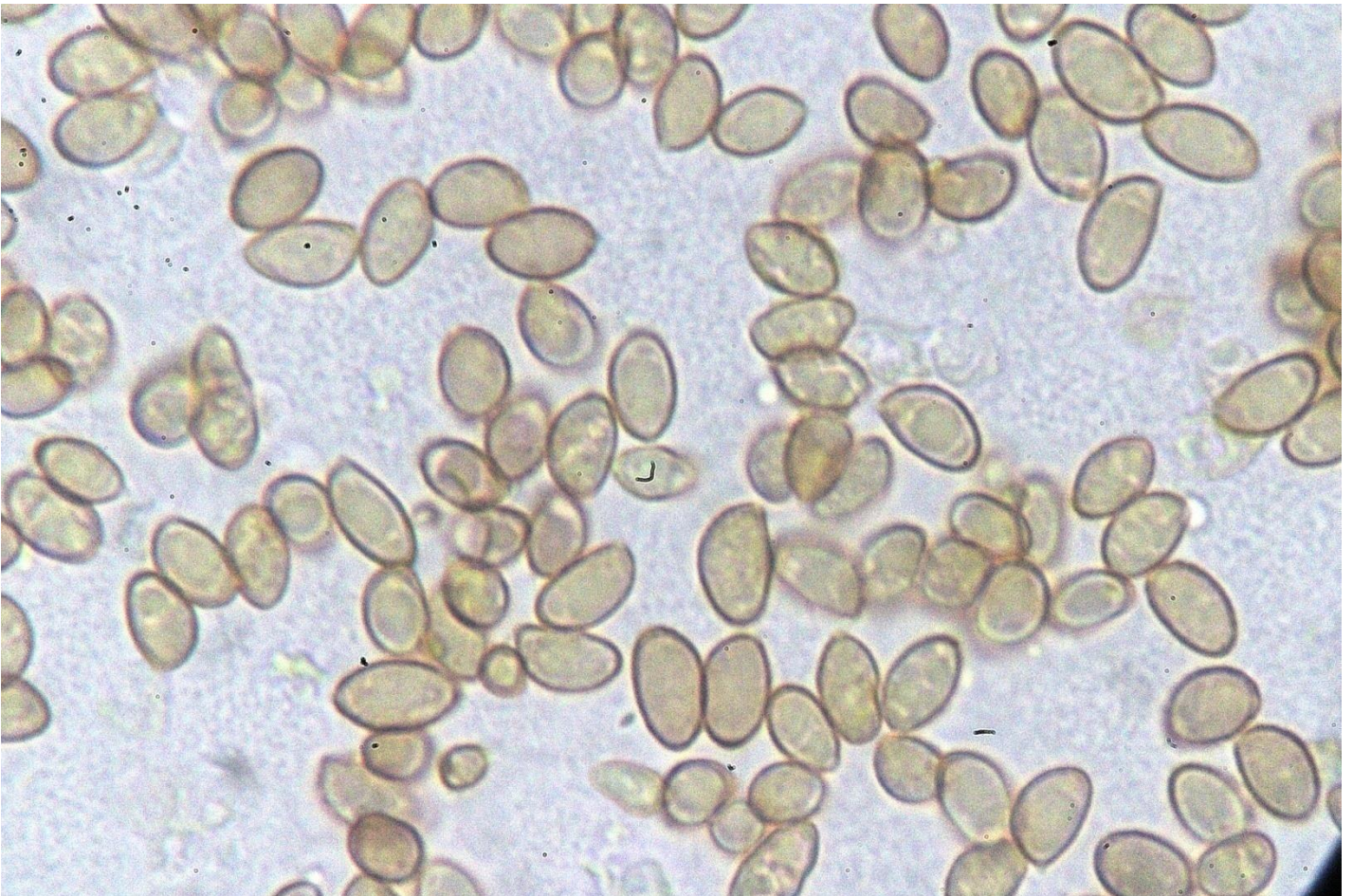
Cortinarius aurilicis Chevassut & Trescol



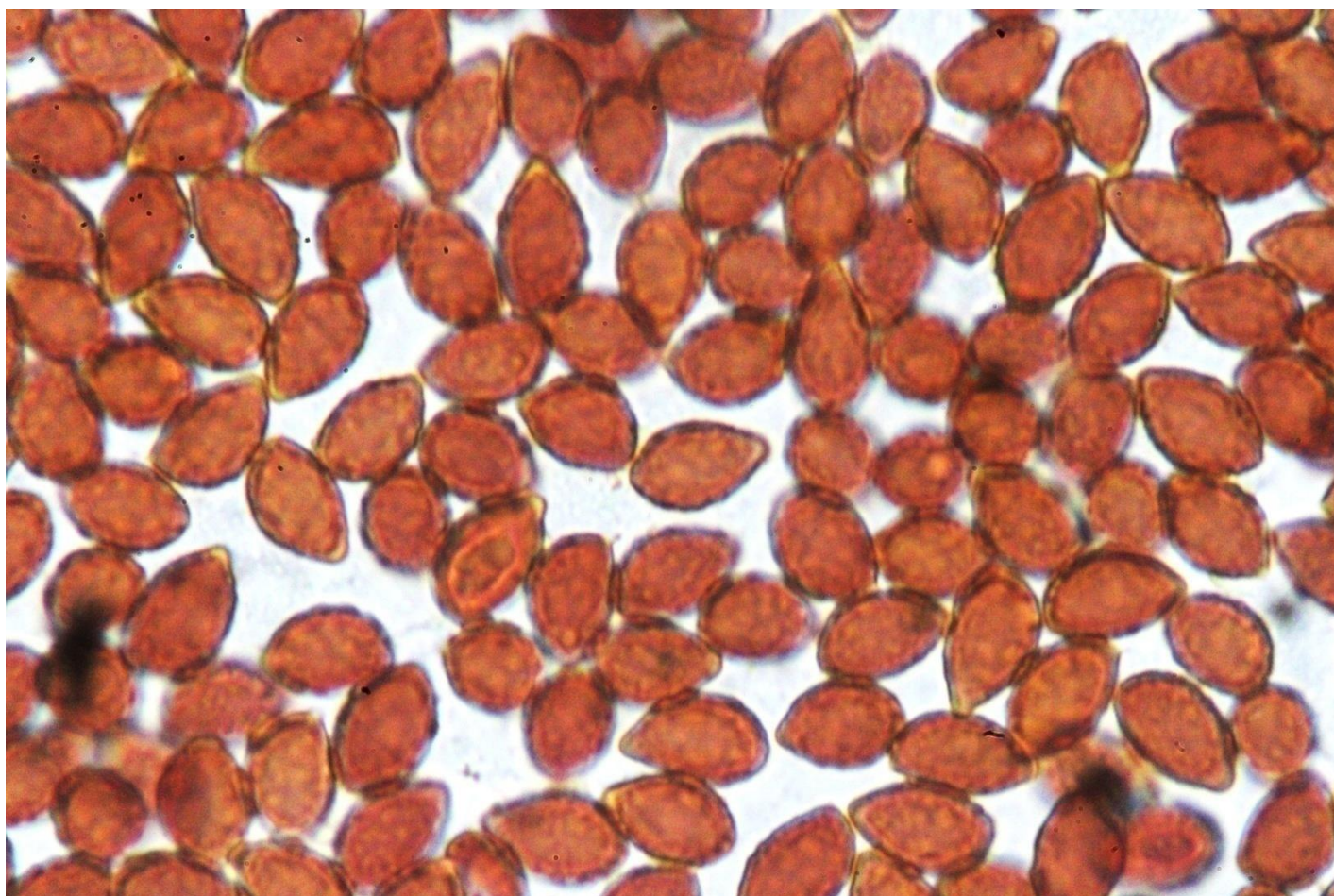
Cortinarius bolaris (Pers.) Zaw.



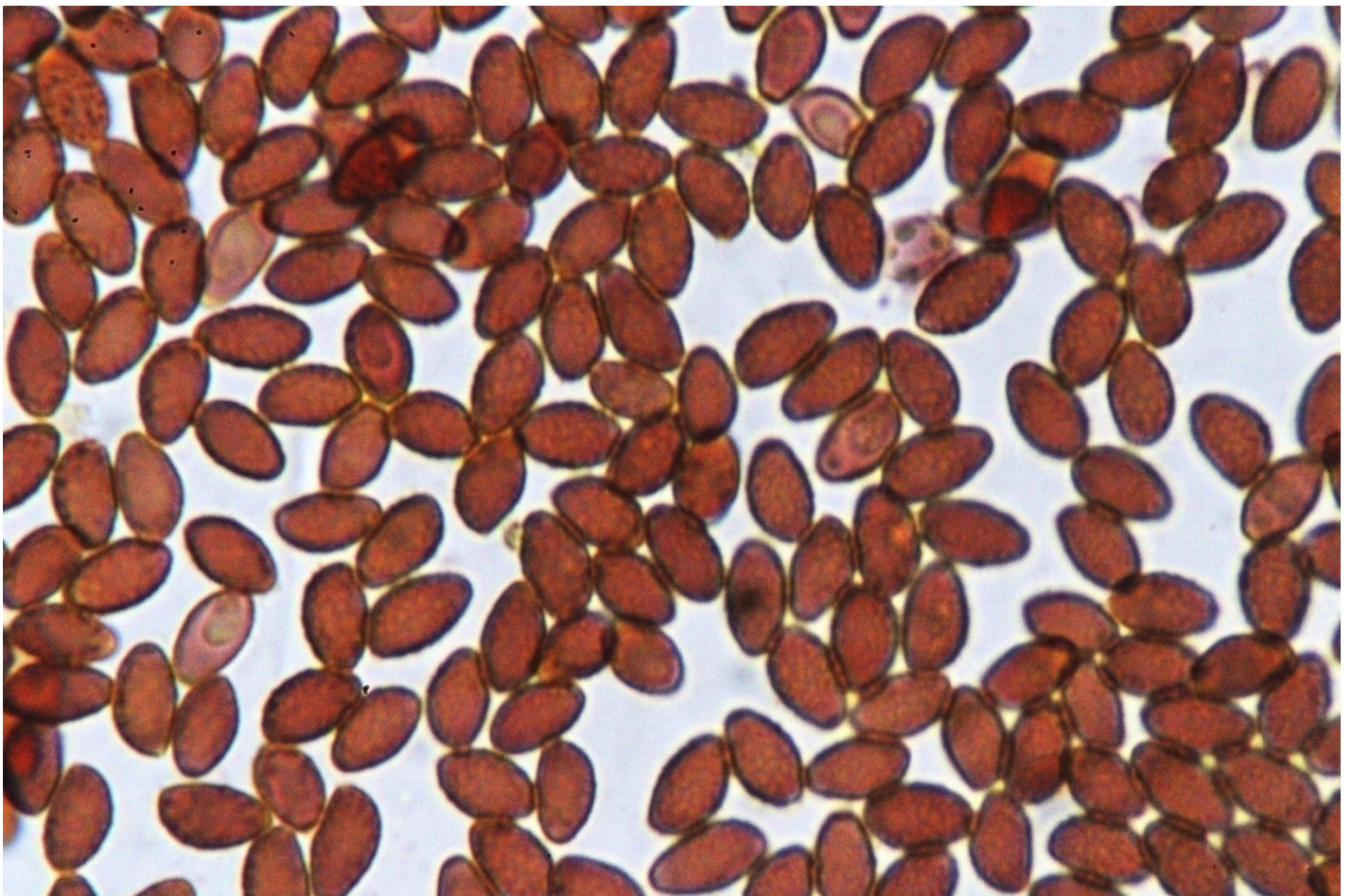
Cortinarius caligatus Malençon



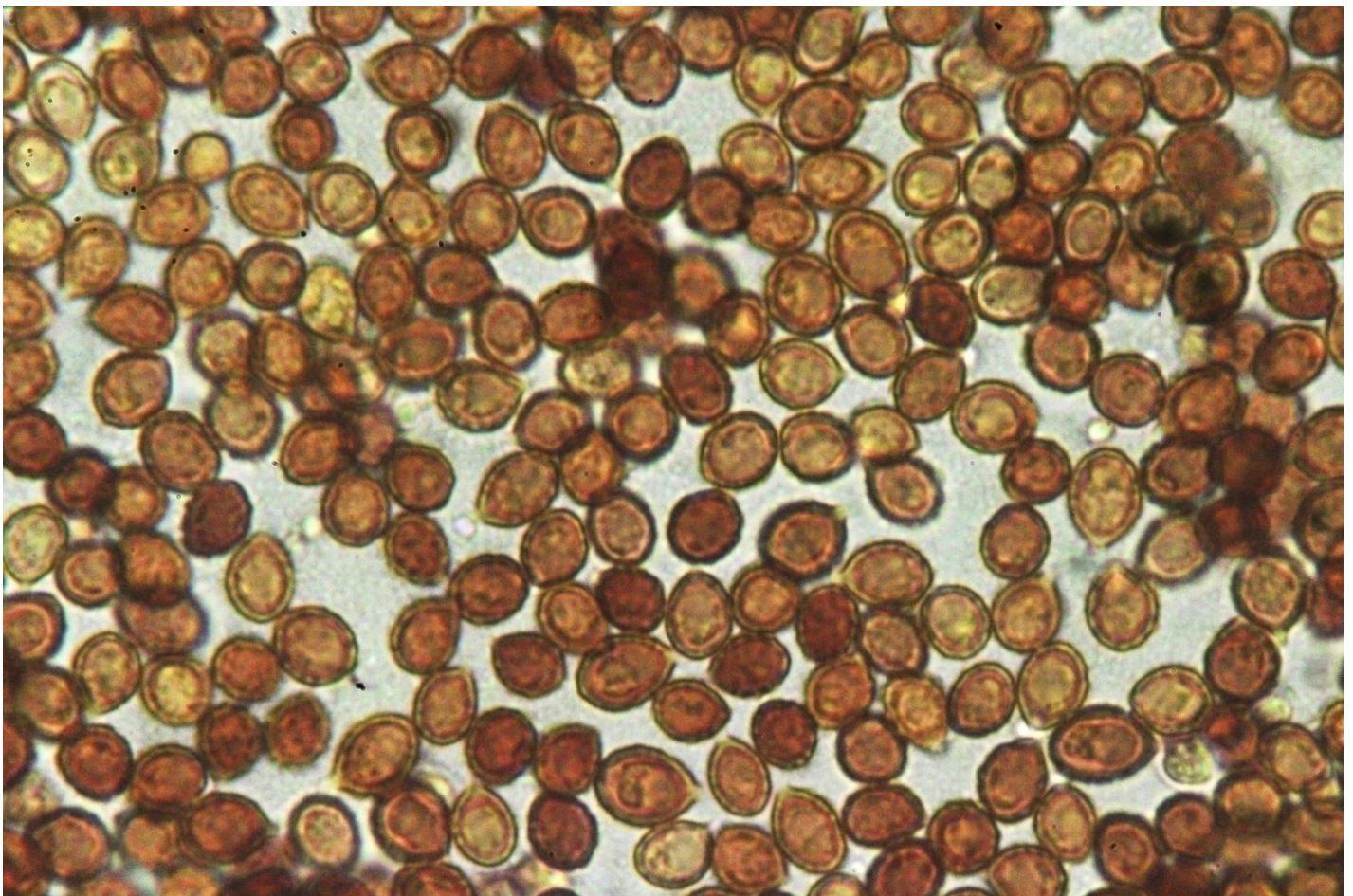
Cortinarius camphoratus (Fr.) Fr.



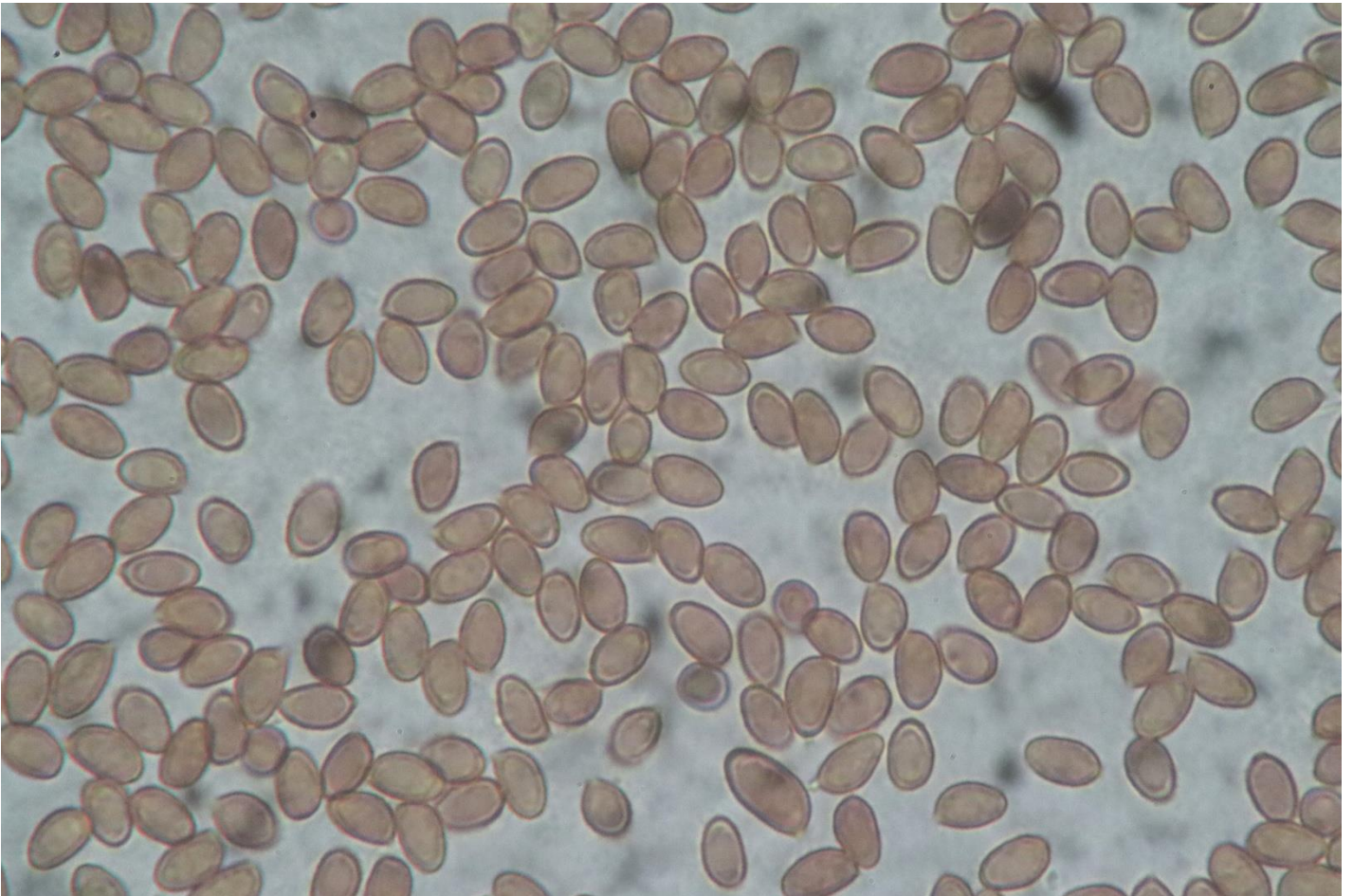
Cortinarius cedretorum Maire



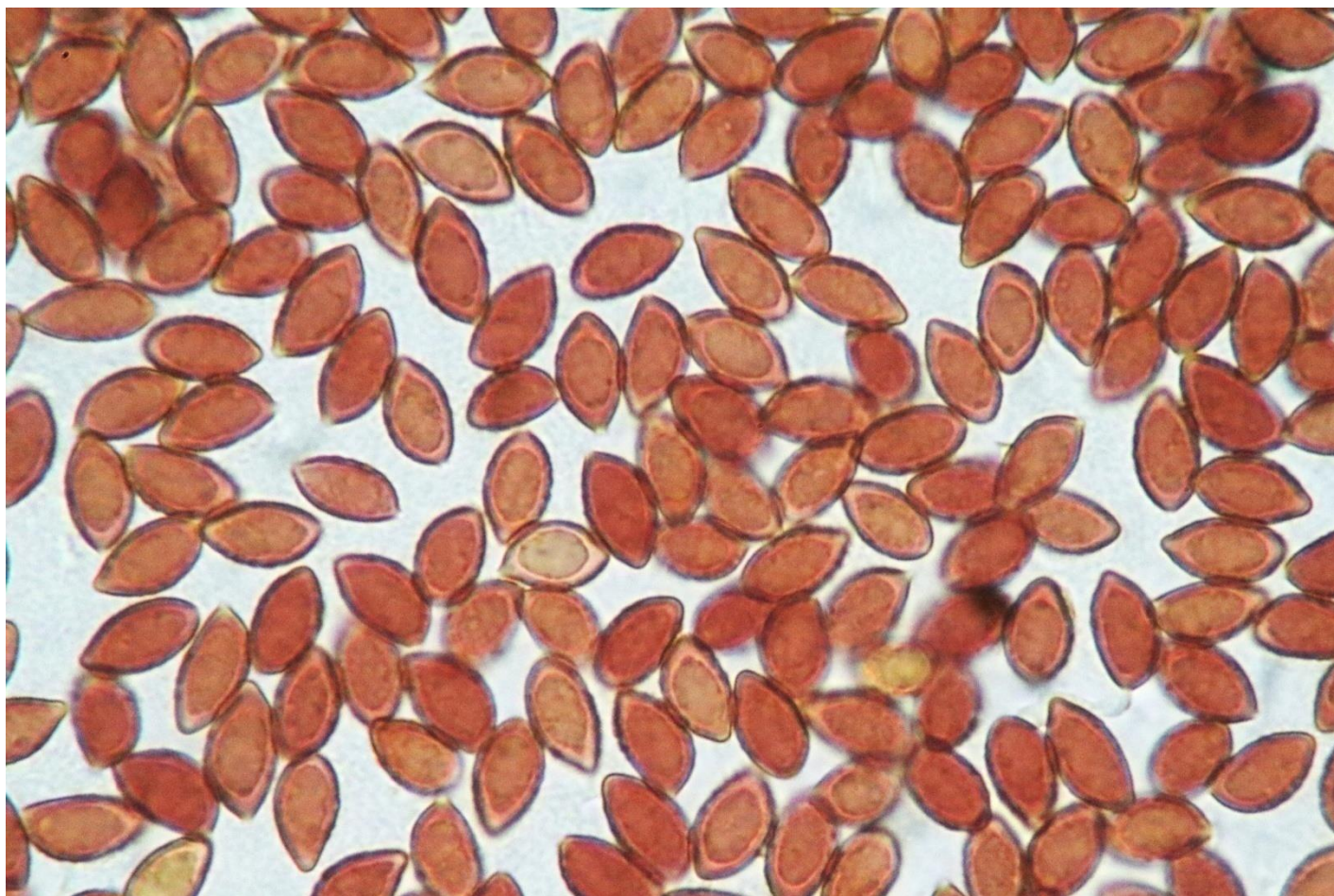
Cortinarius cystoglaucopus A. Ortega, Vila, J.C. Campos & Fern.-Brime



Cortinarius cotoneus Fr.



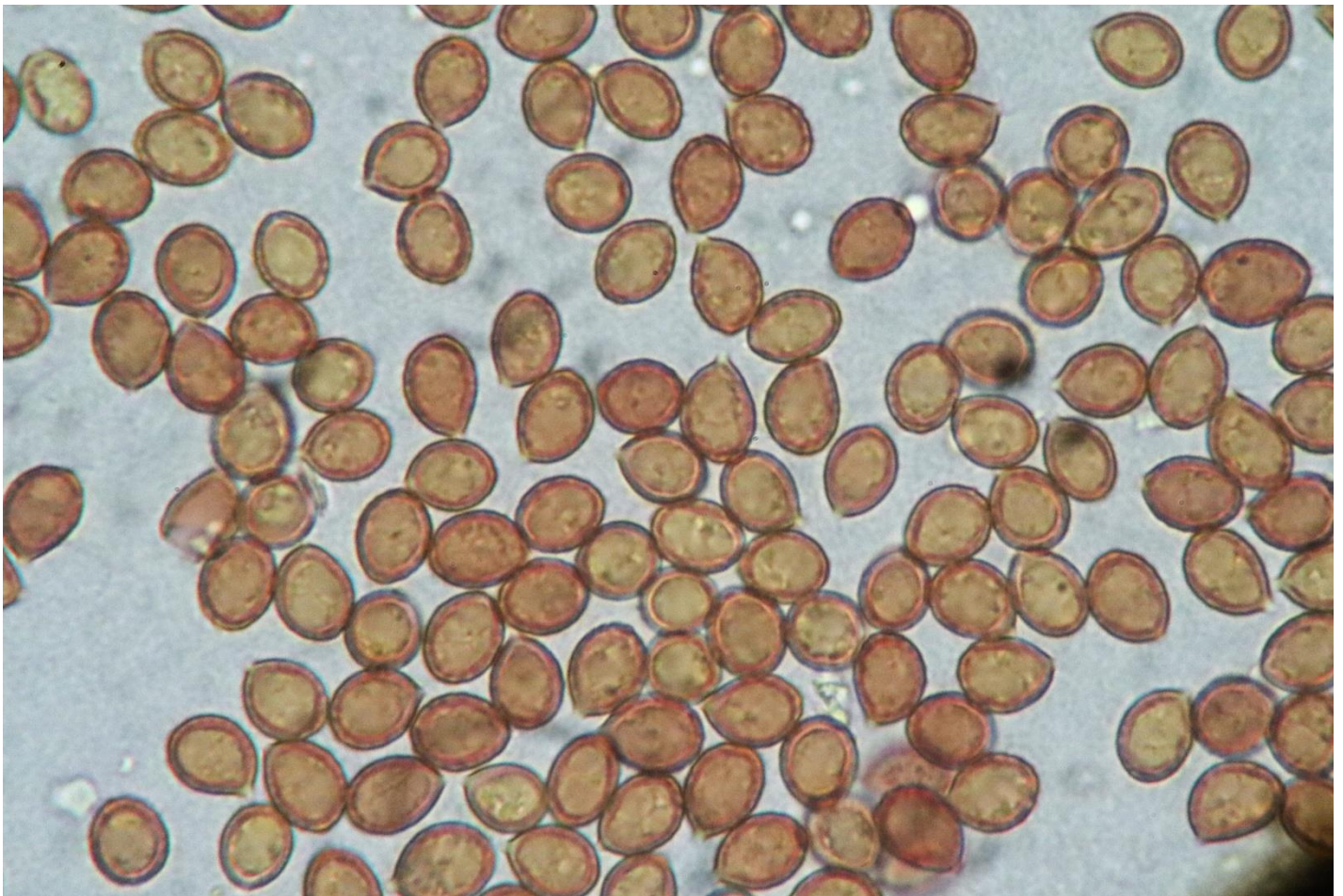
Cortinarius crystallinus Fr.



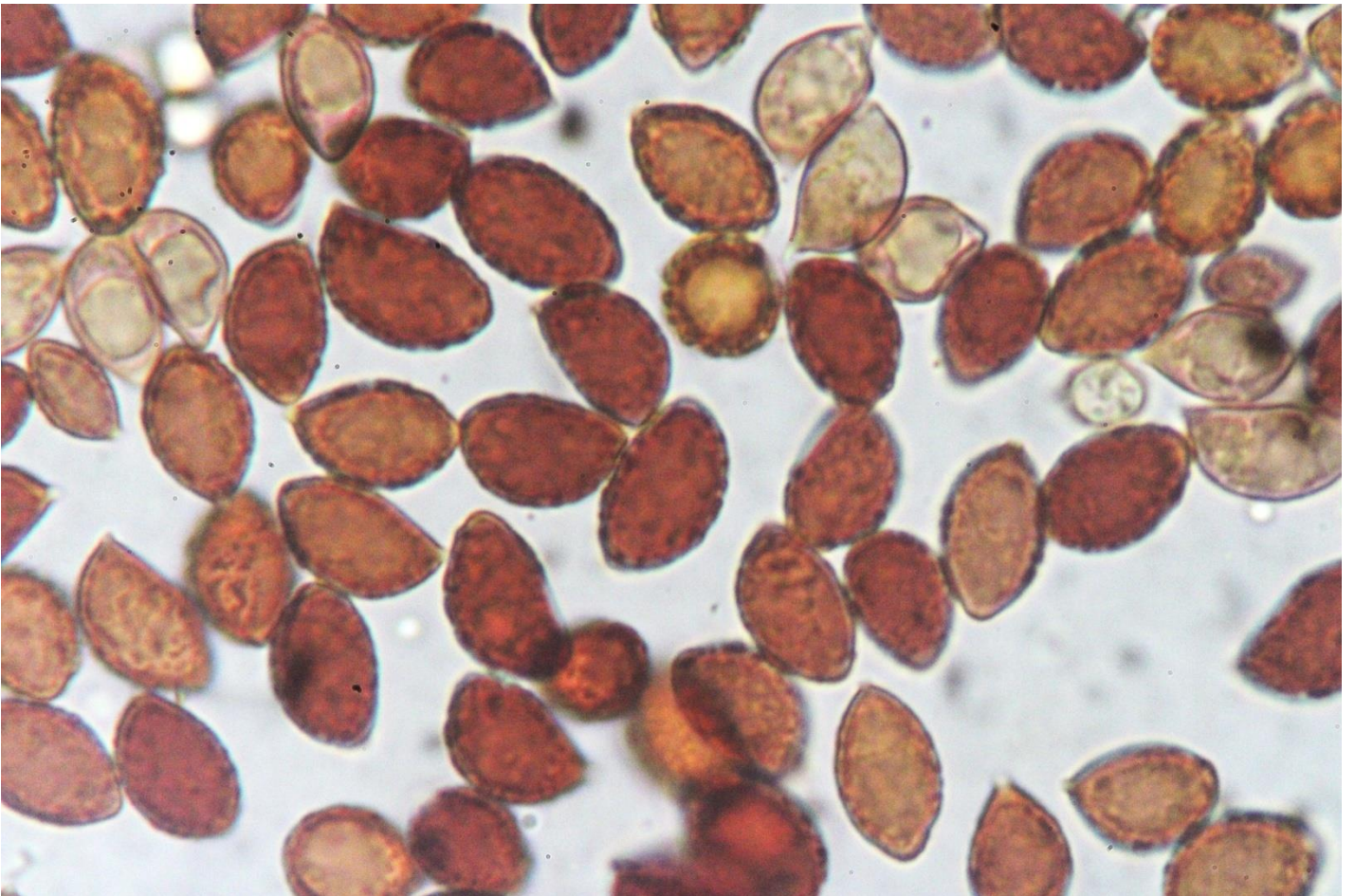
Cortinarius dibaphus Fr.



NCS S 4030-y30r



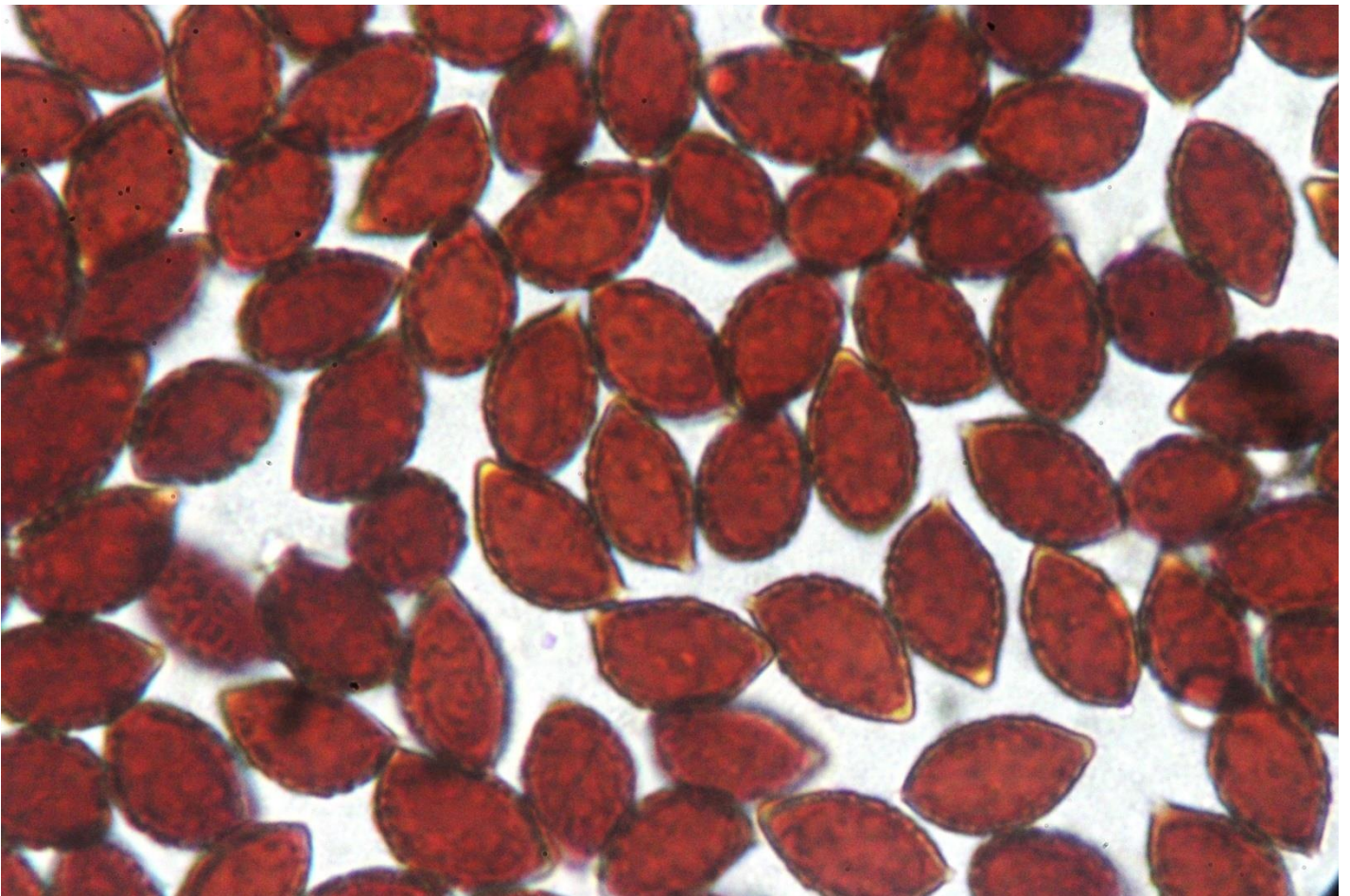
Cortinarius dryosalor Armada, Bidaud, Bellanger & Loizides



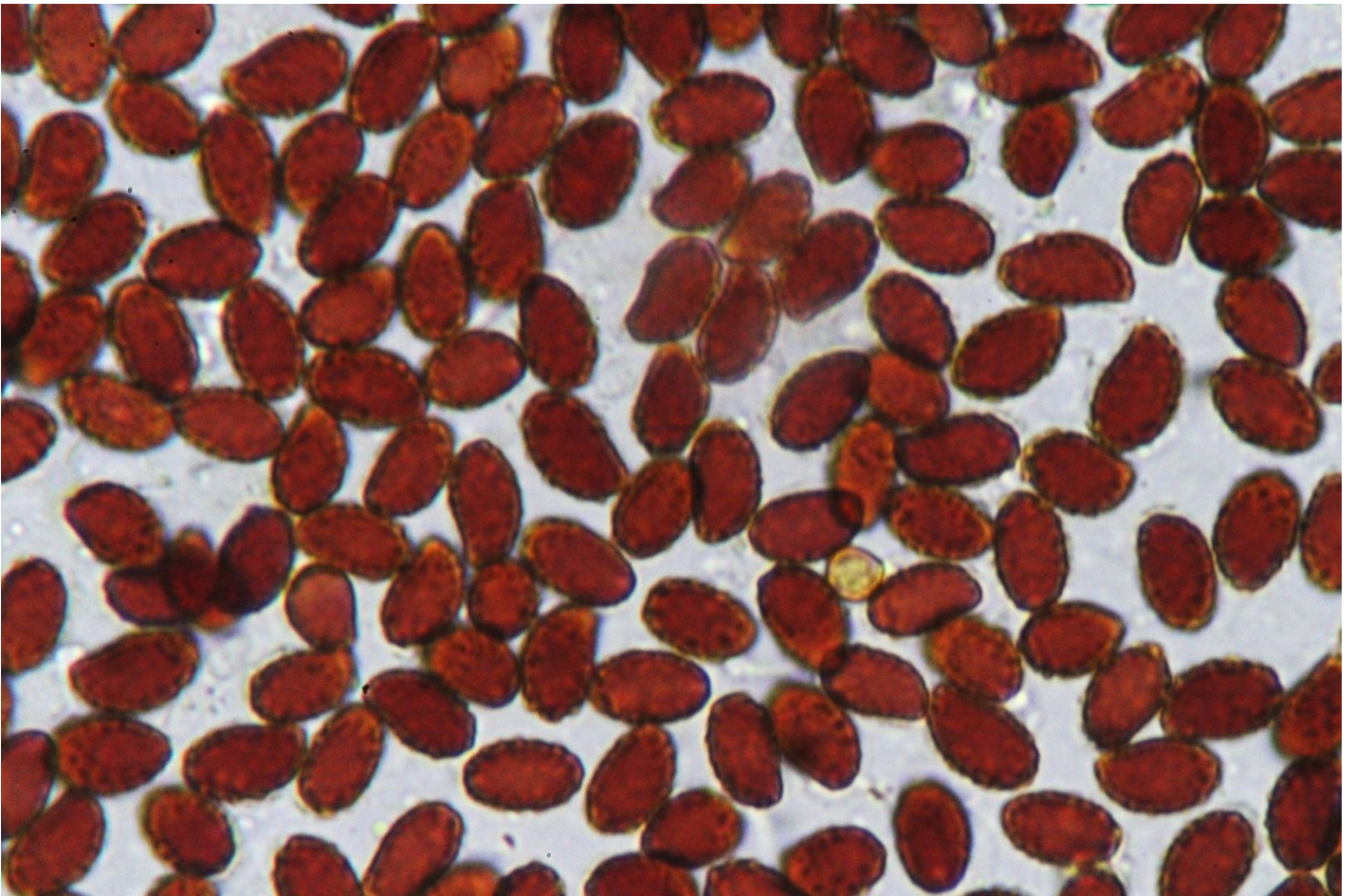
Cortinarius elatior Fr.



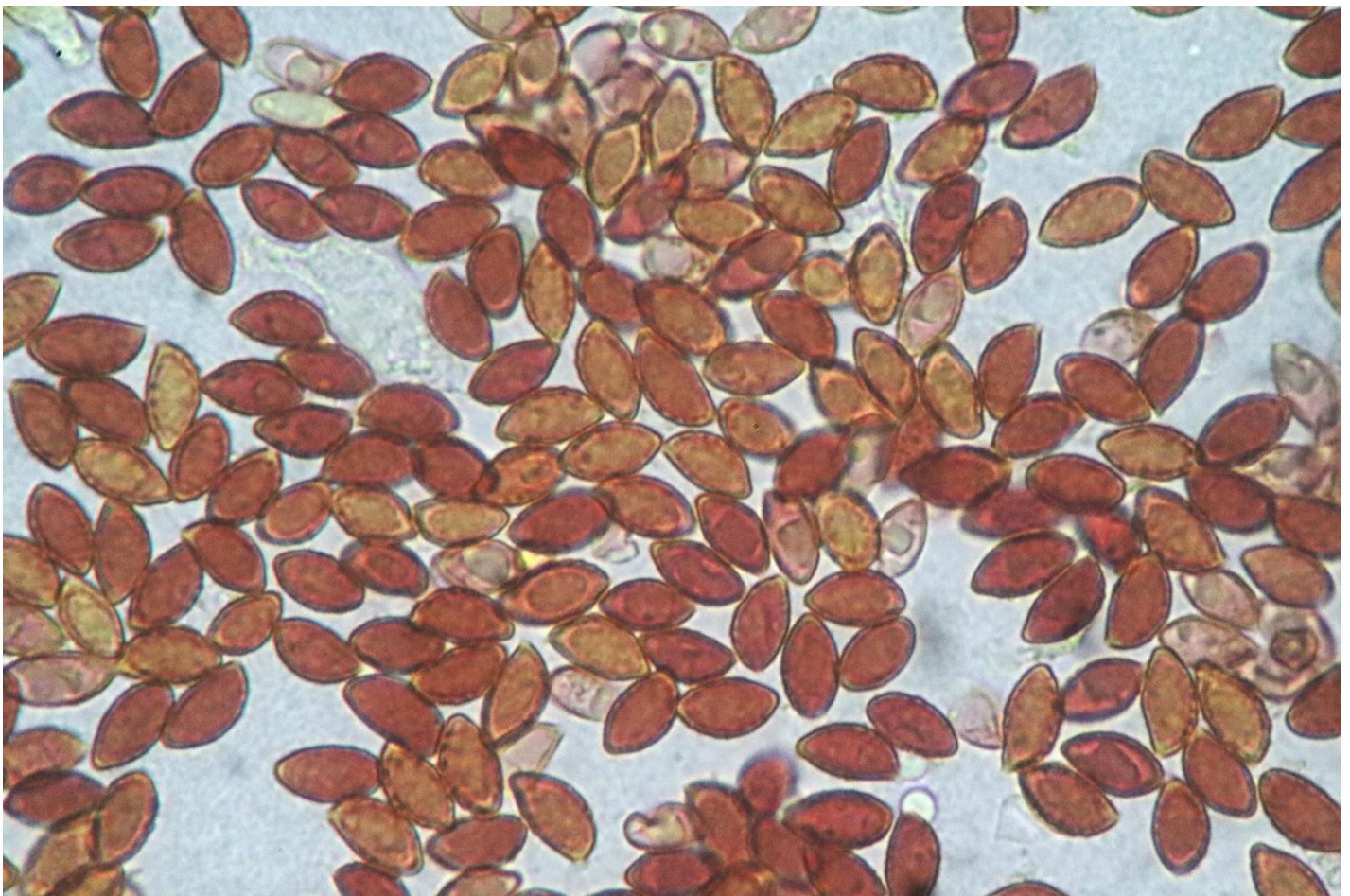
NCS S 5040-y80r



Cortinarius elegantissimus Rob. Henry



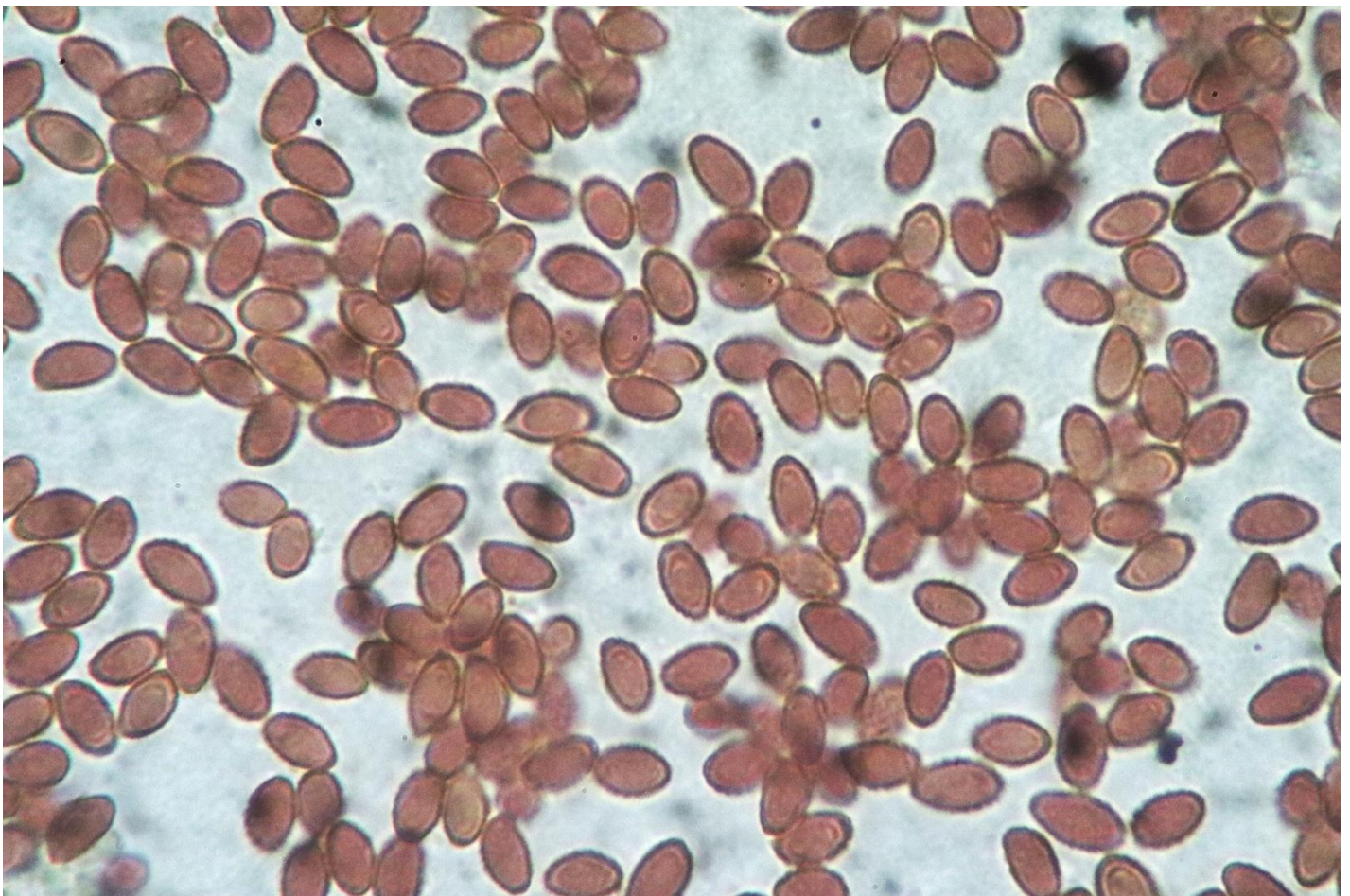
Cortinarius epipurpus Chevassut & Rob. Henry



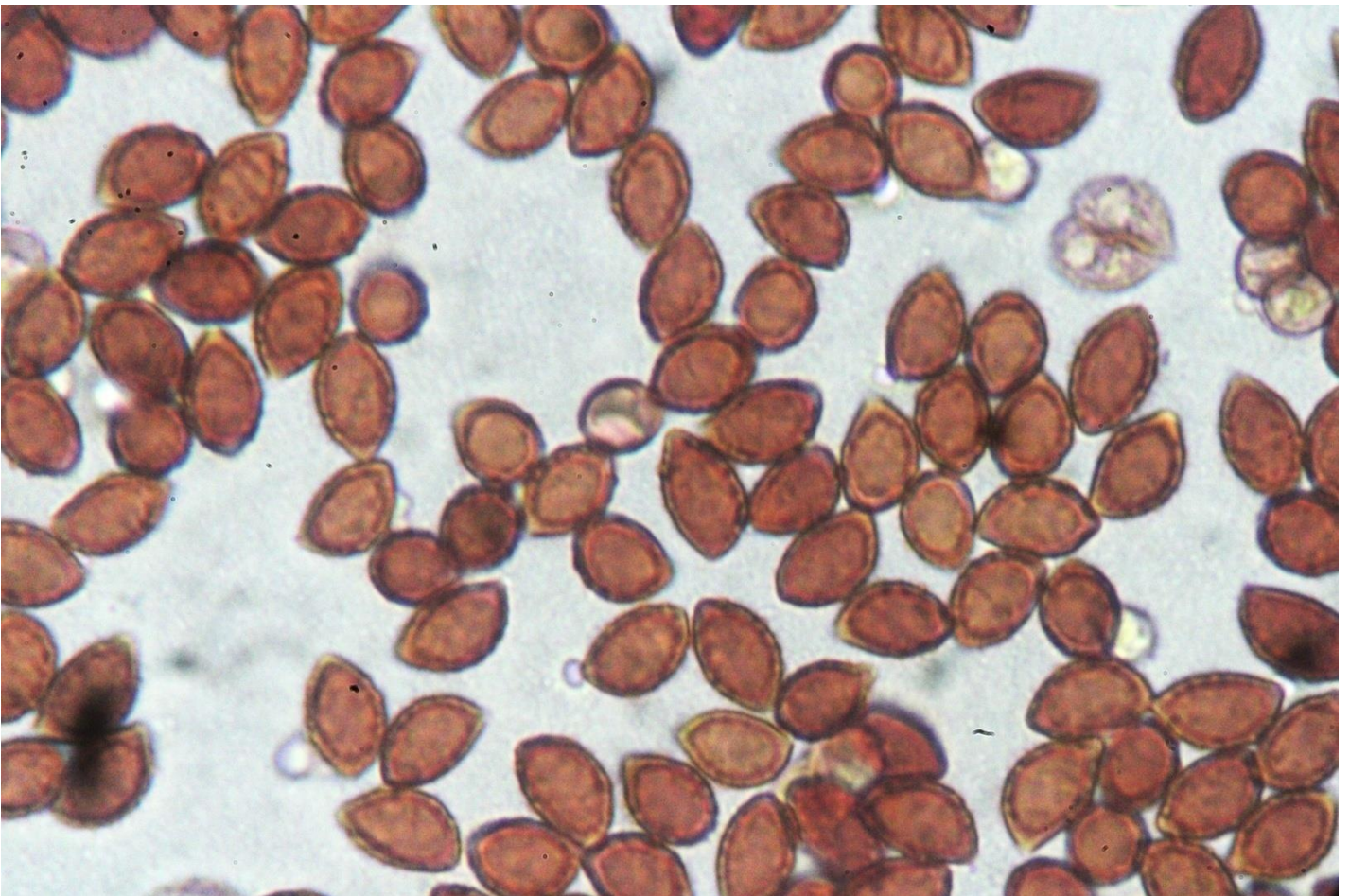
Cortinarius fulminatus Reumaux



NCS S 5020-y80r



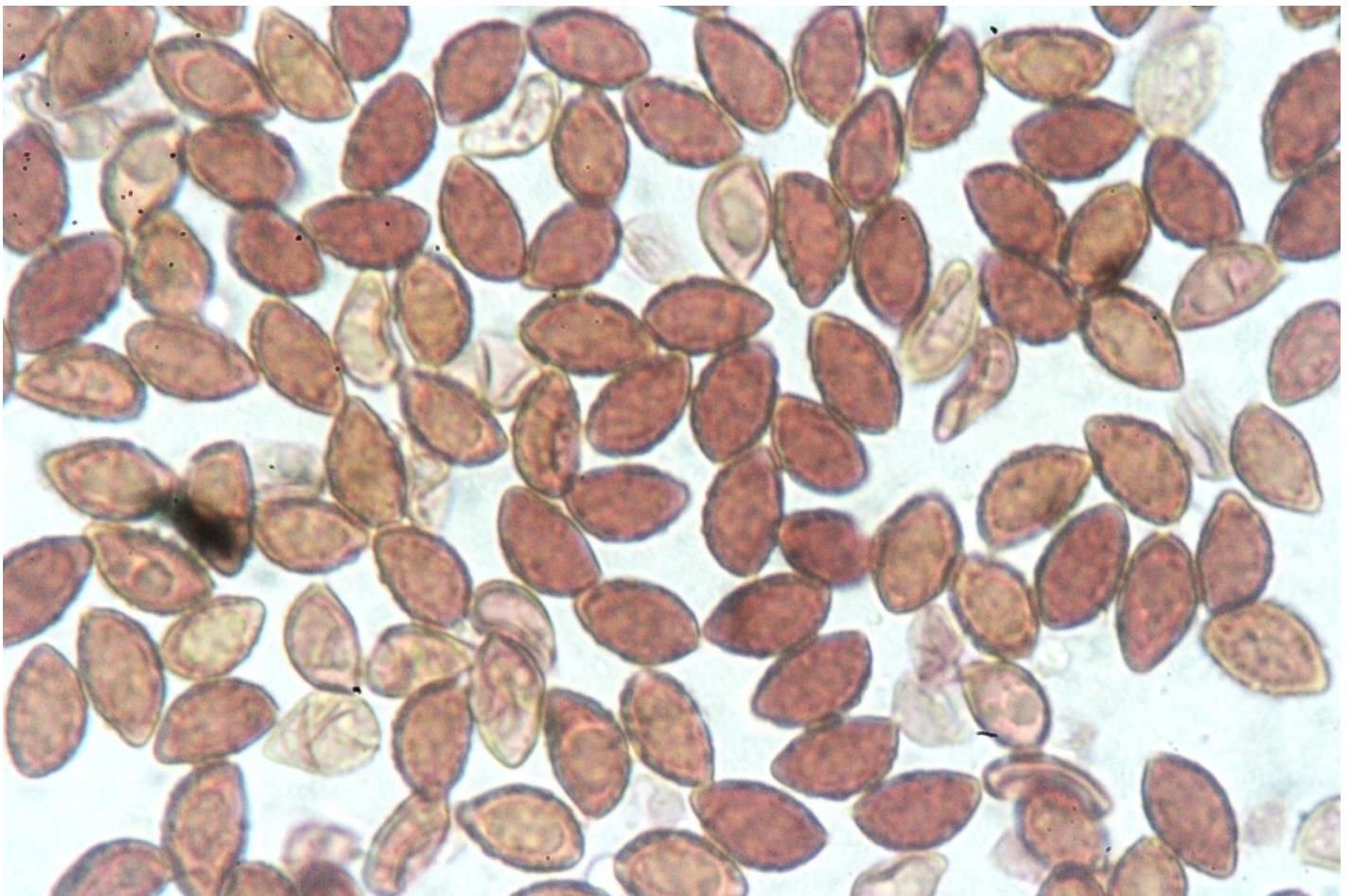
Cortinarius glaucopus (Schaeff.) Gray



Cortinarius ionochlorus Maire



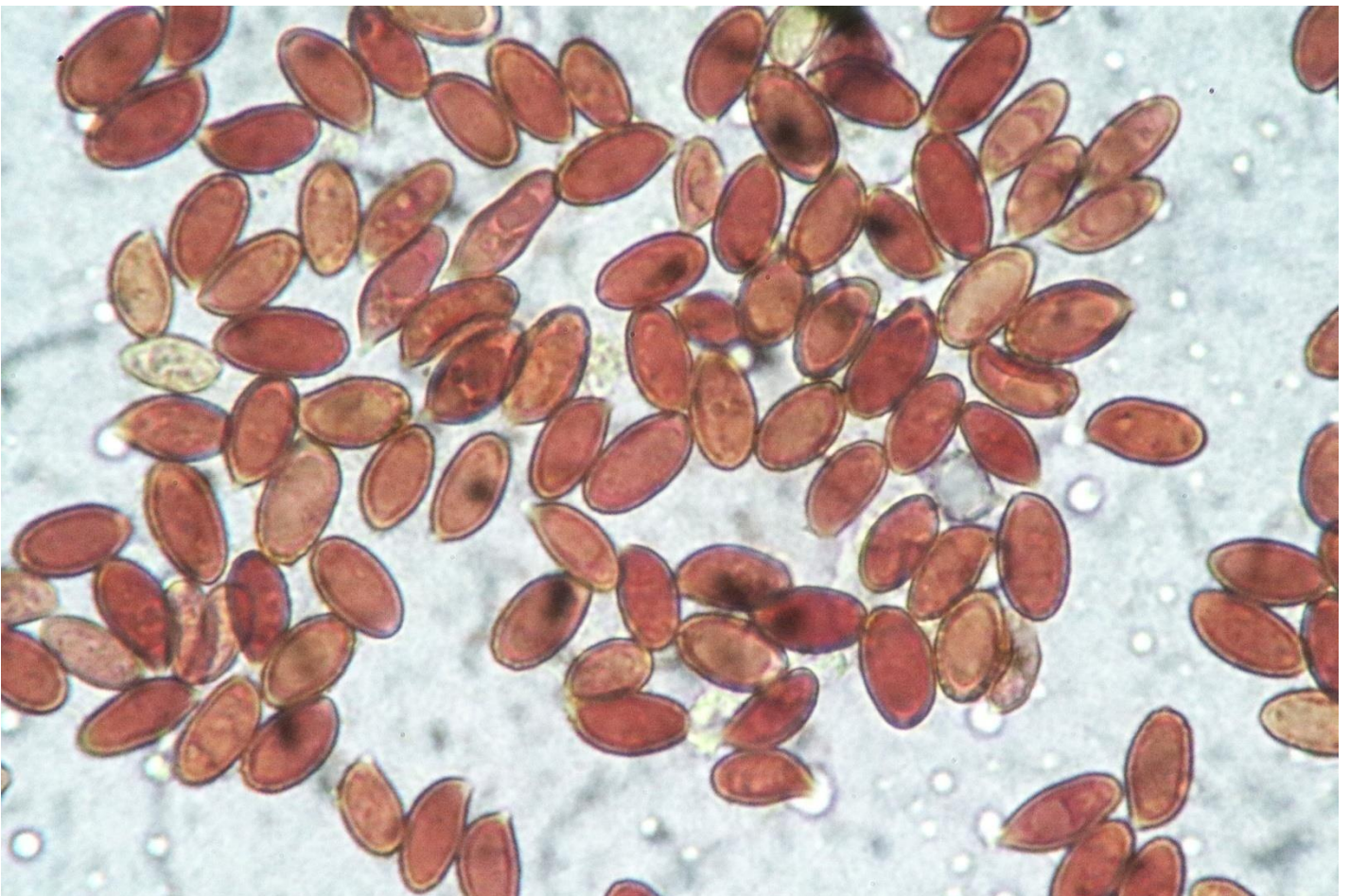
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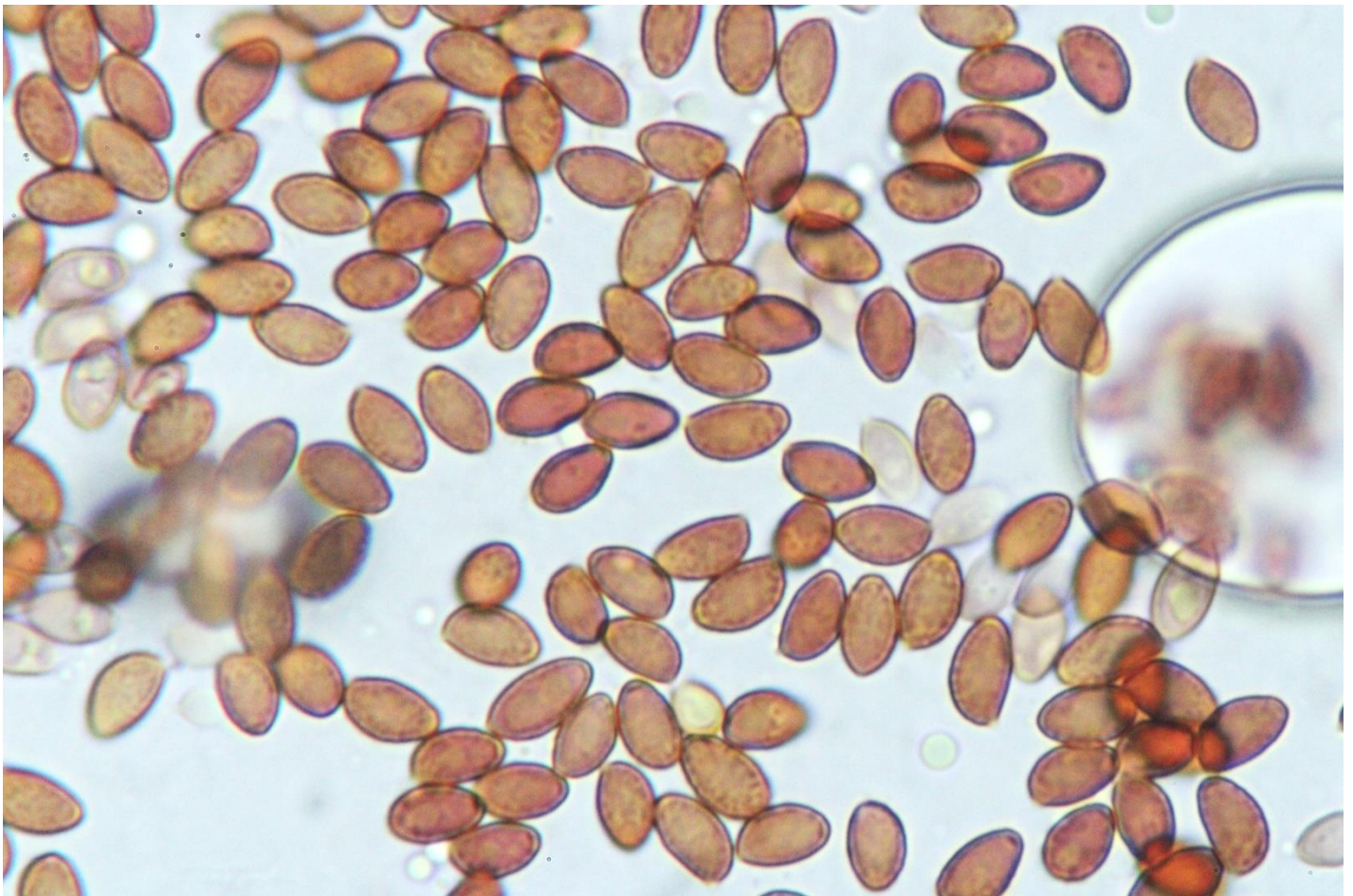
Cortinarius joguetii Melot



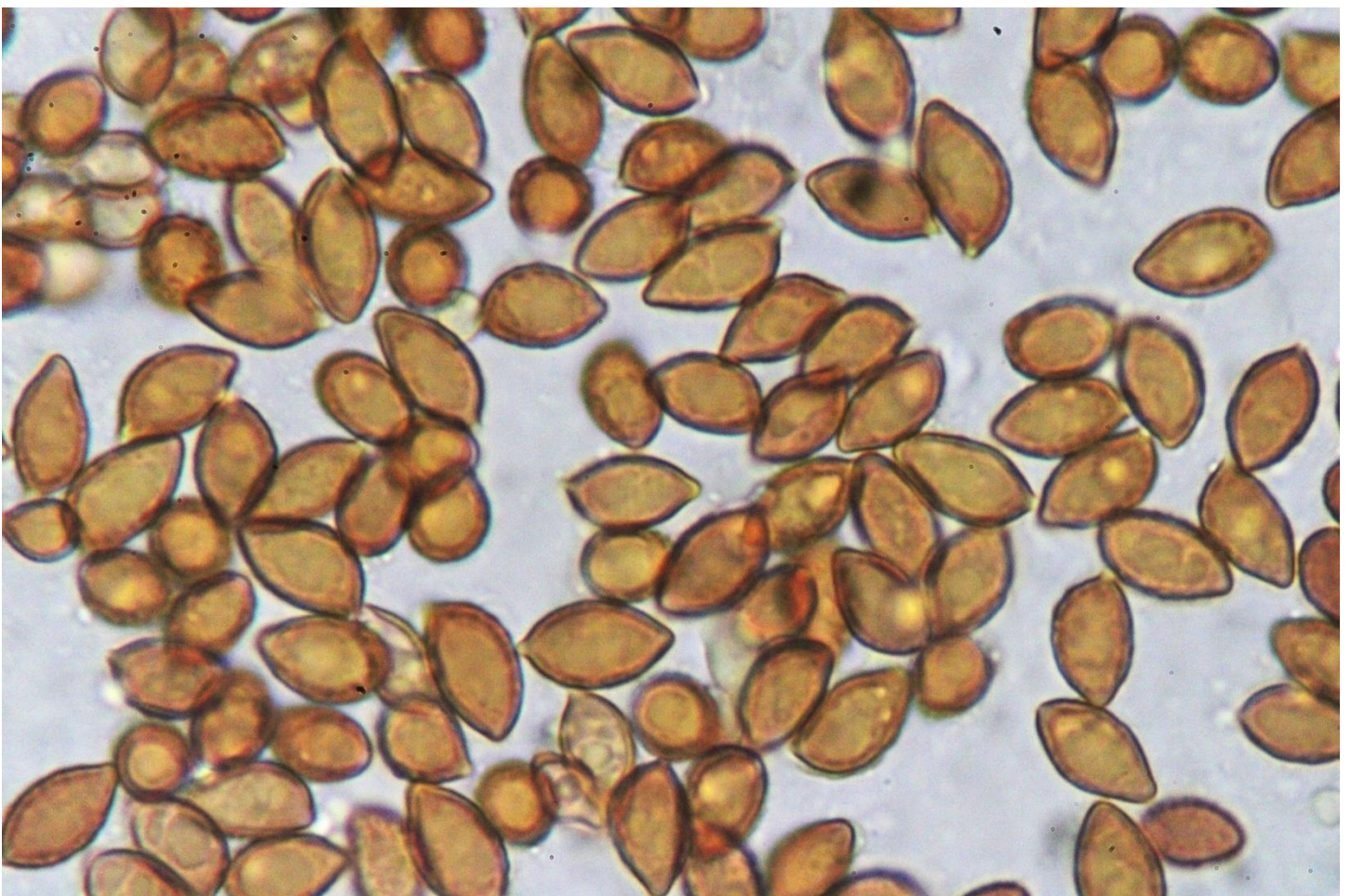
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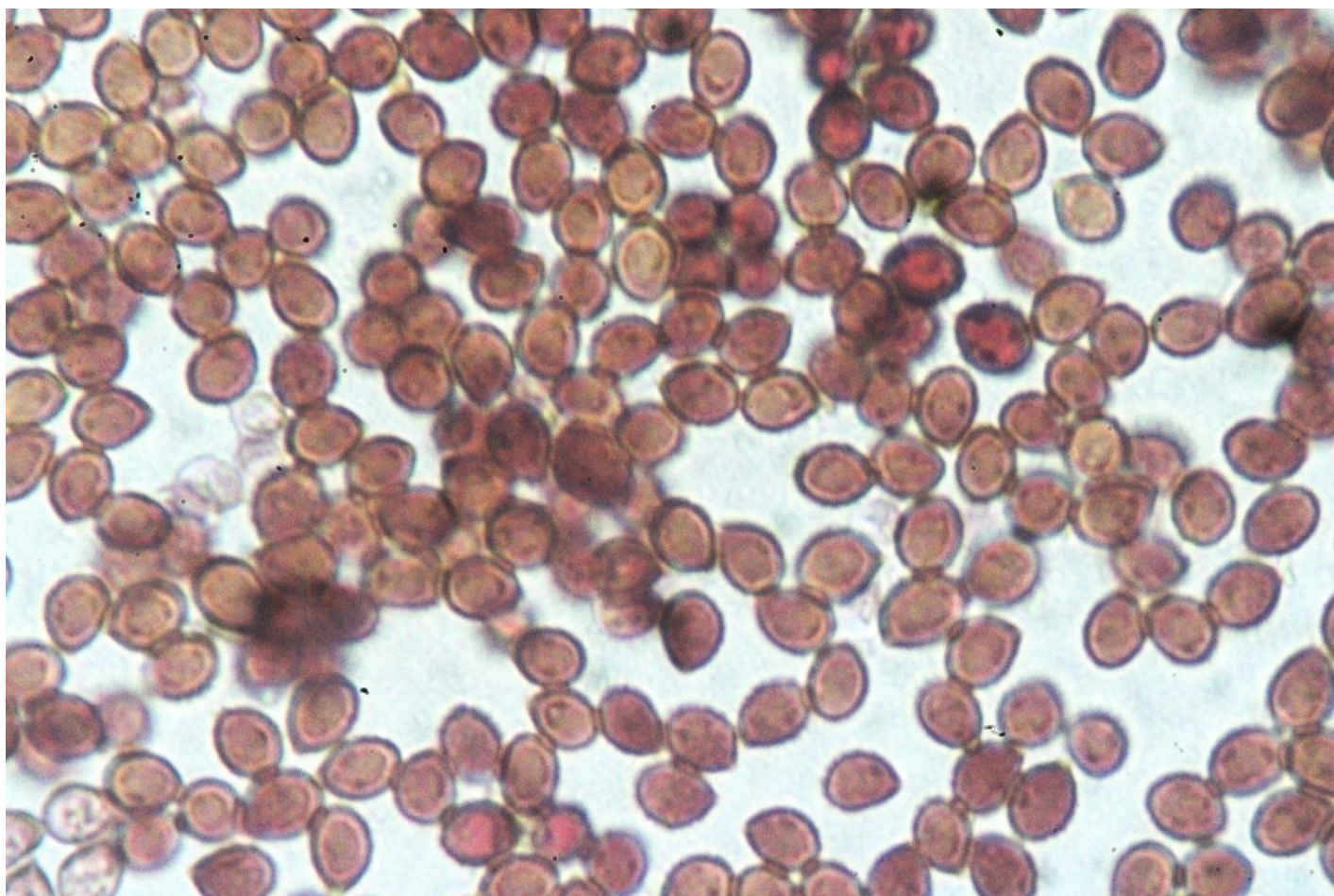
Cortinarius laniger Fr.



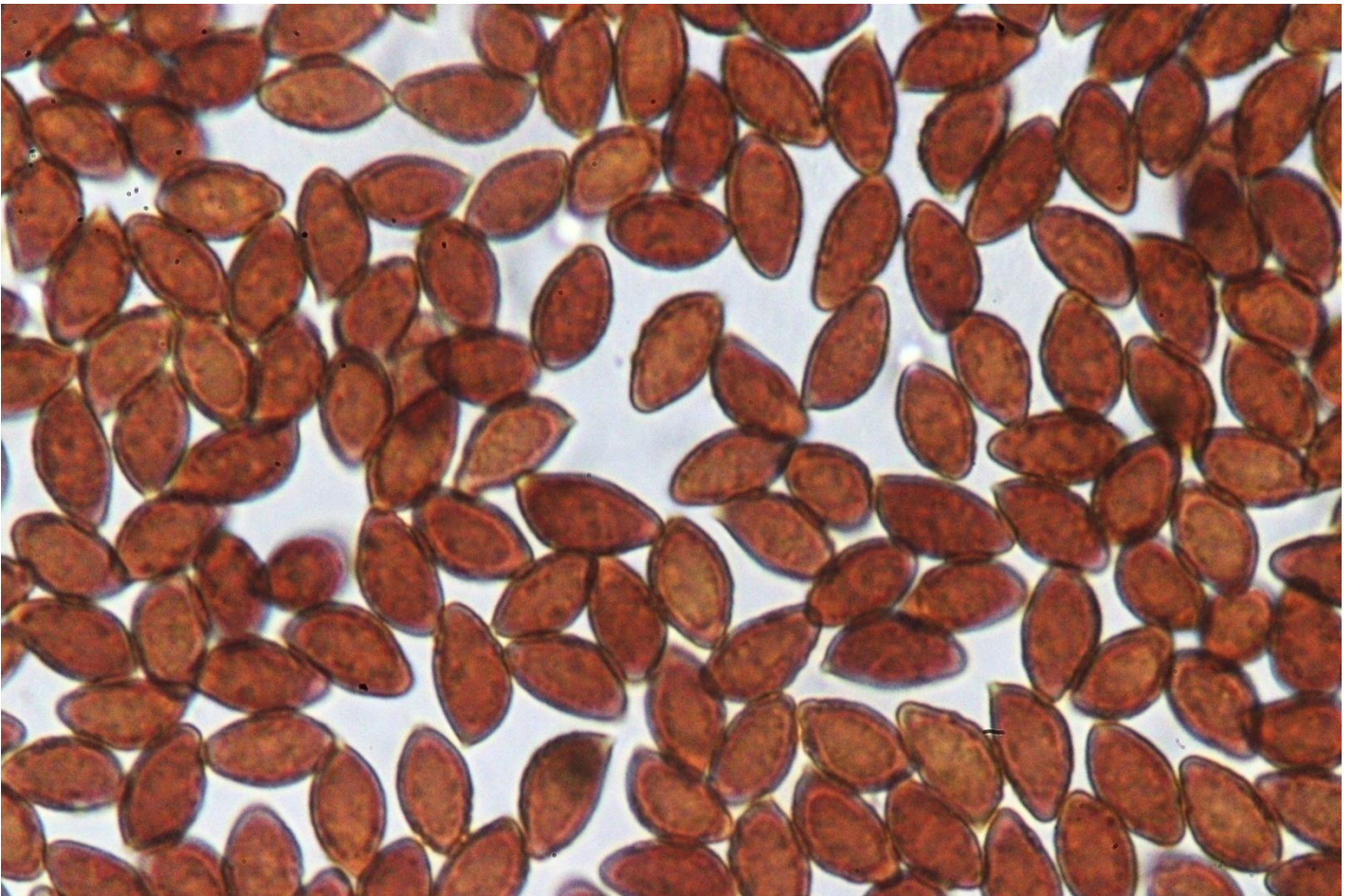
Cortinarius magicus Eichhorn



Cortinarius meinhardii Bon



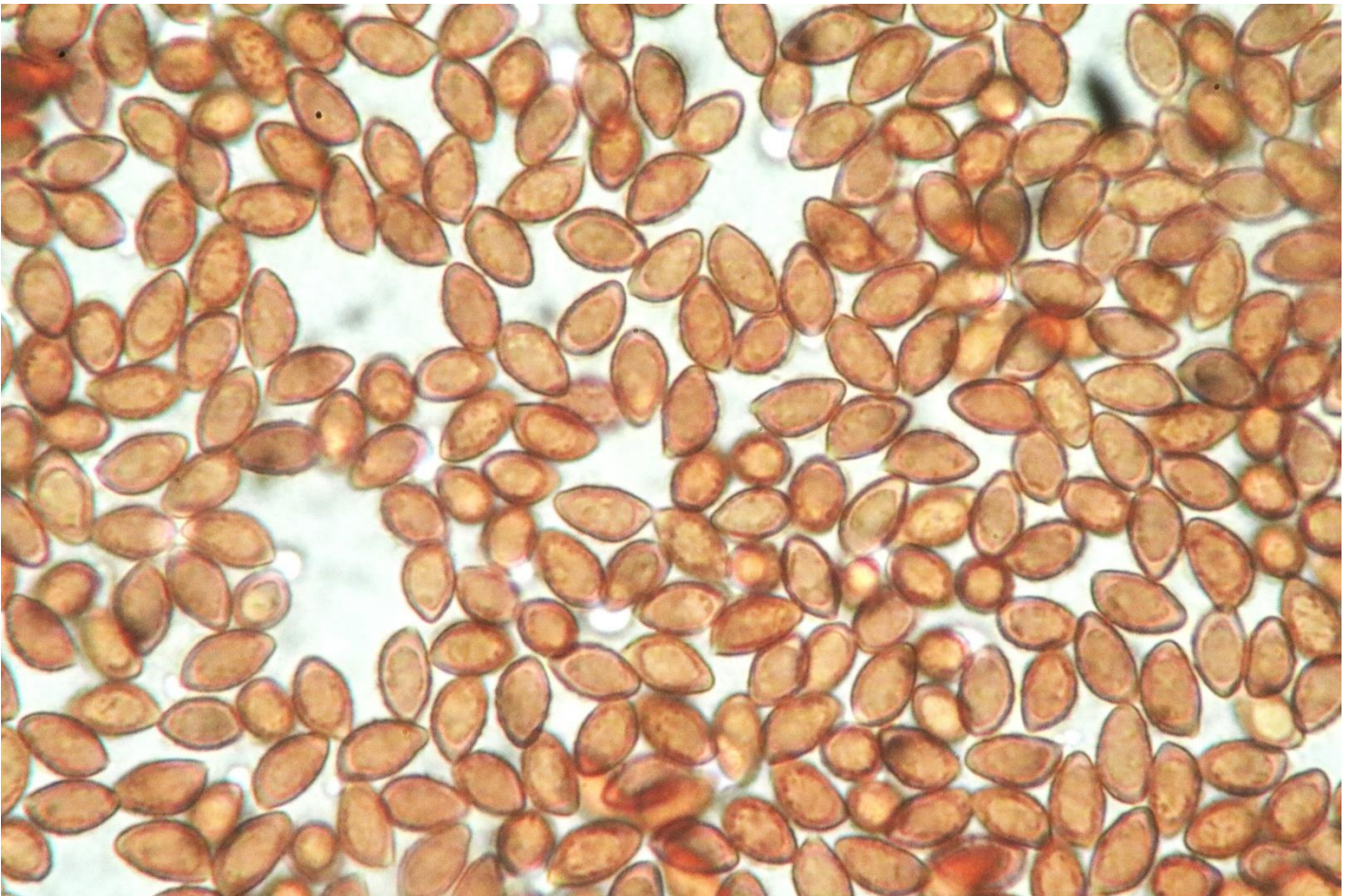
Cortinarius melanotus Kalchbr.



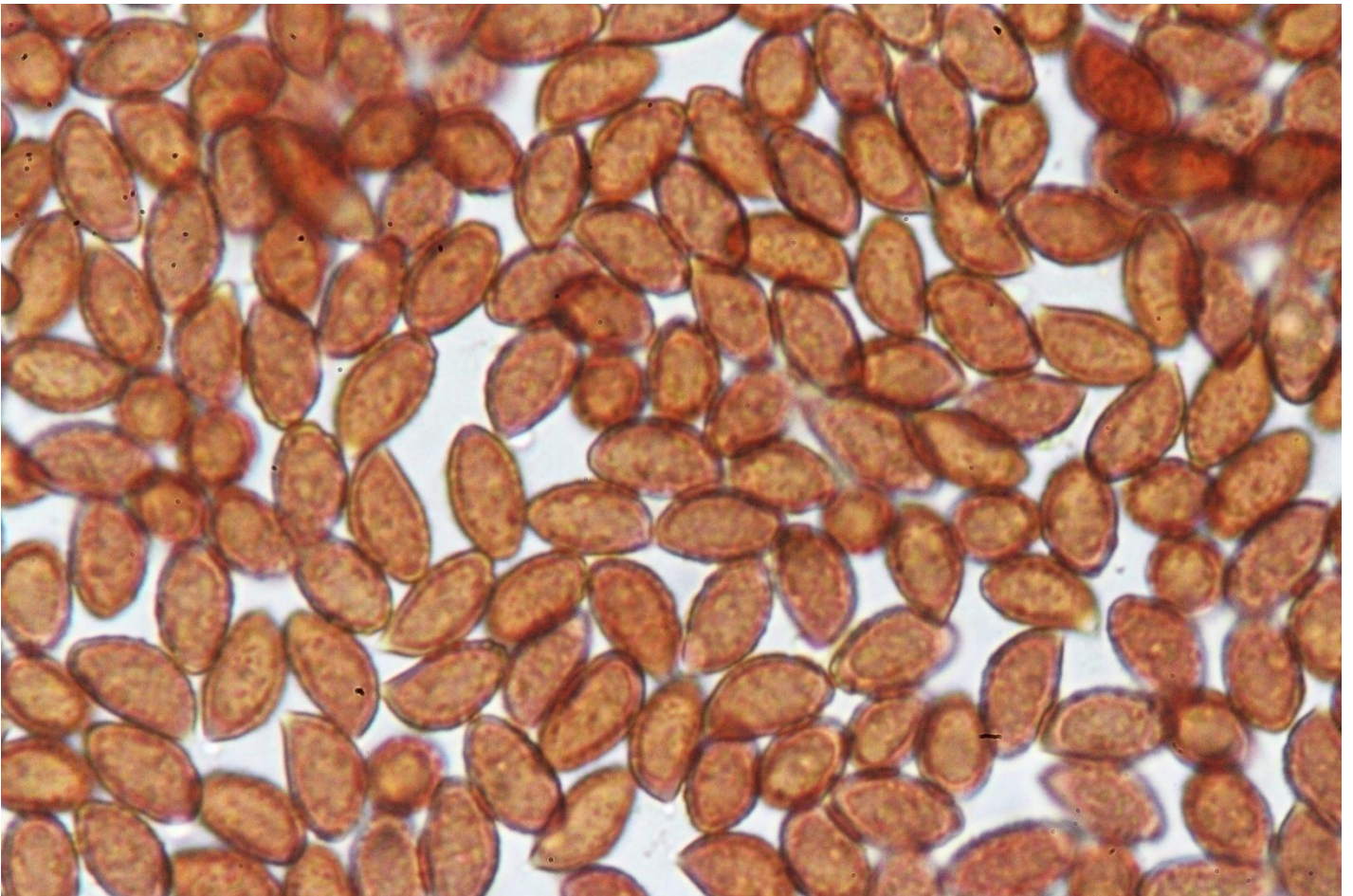
Cortinarius muricinoides Reumaux & Moëne-Locc.



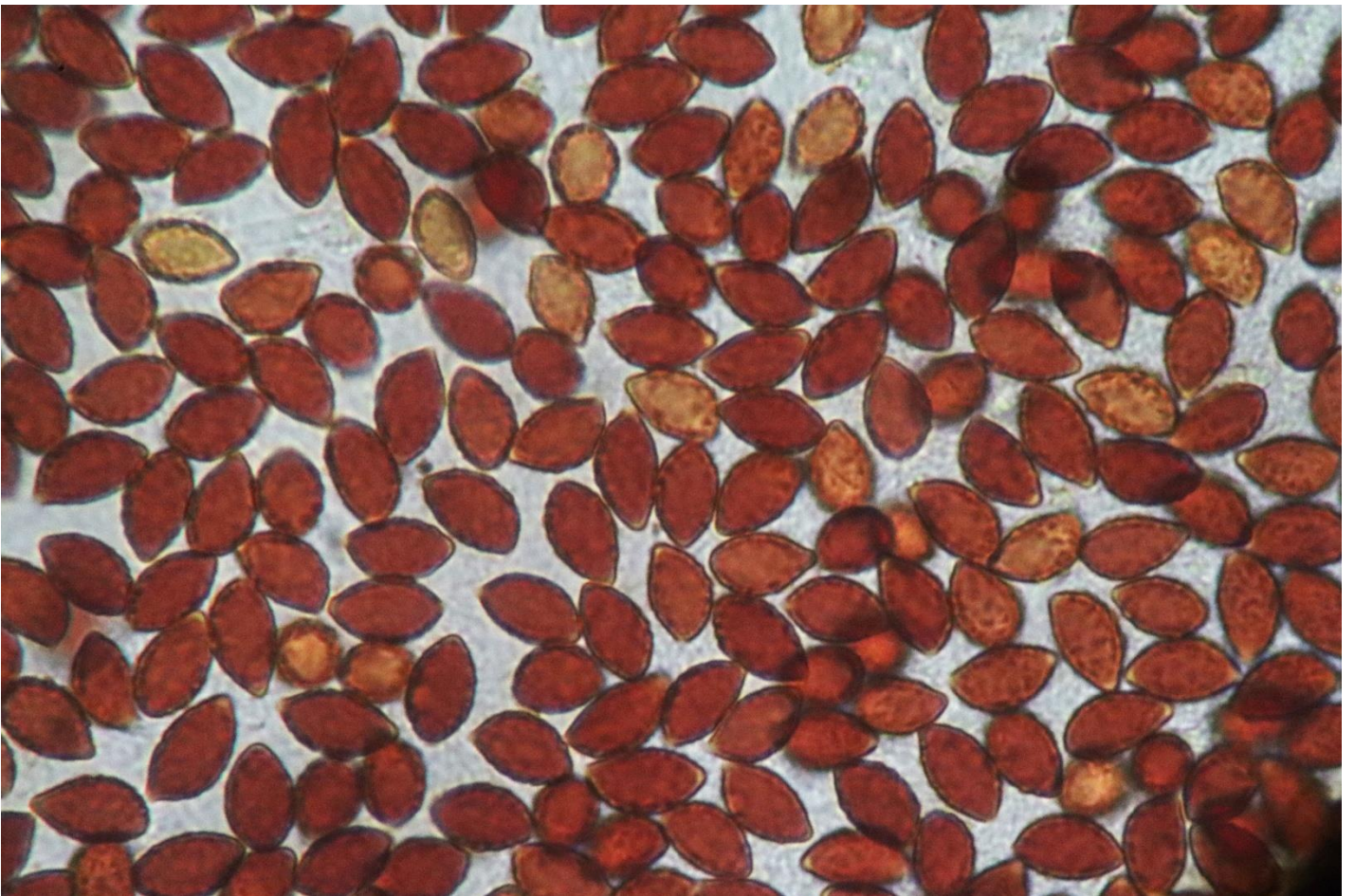
NCS S 1030-y30r



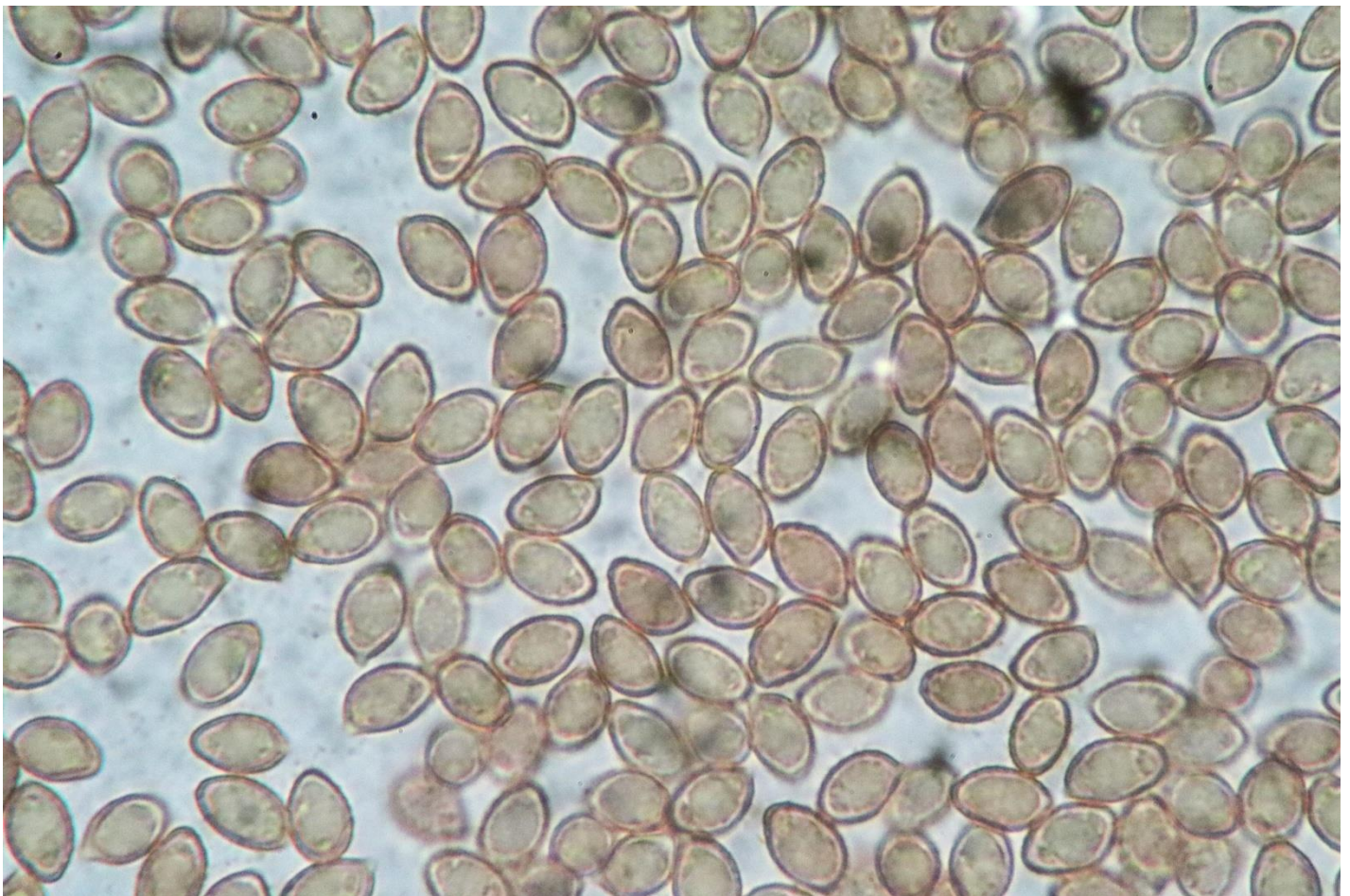
Cortinarius nymphicolor Reumaux



Cortinarius olidus J.E. Lange



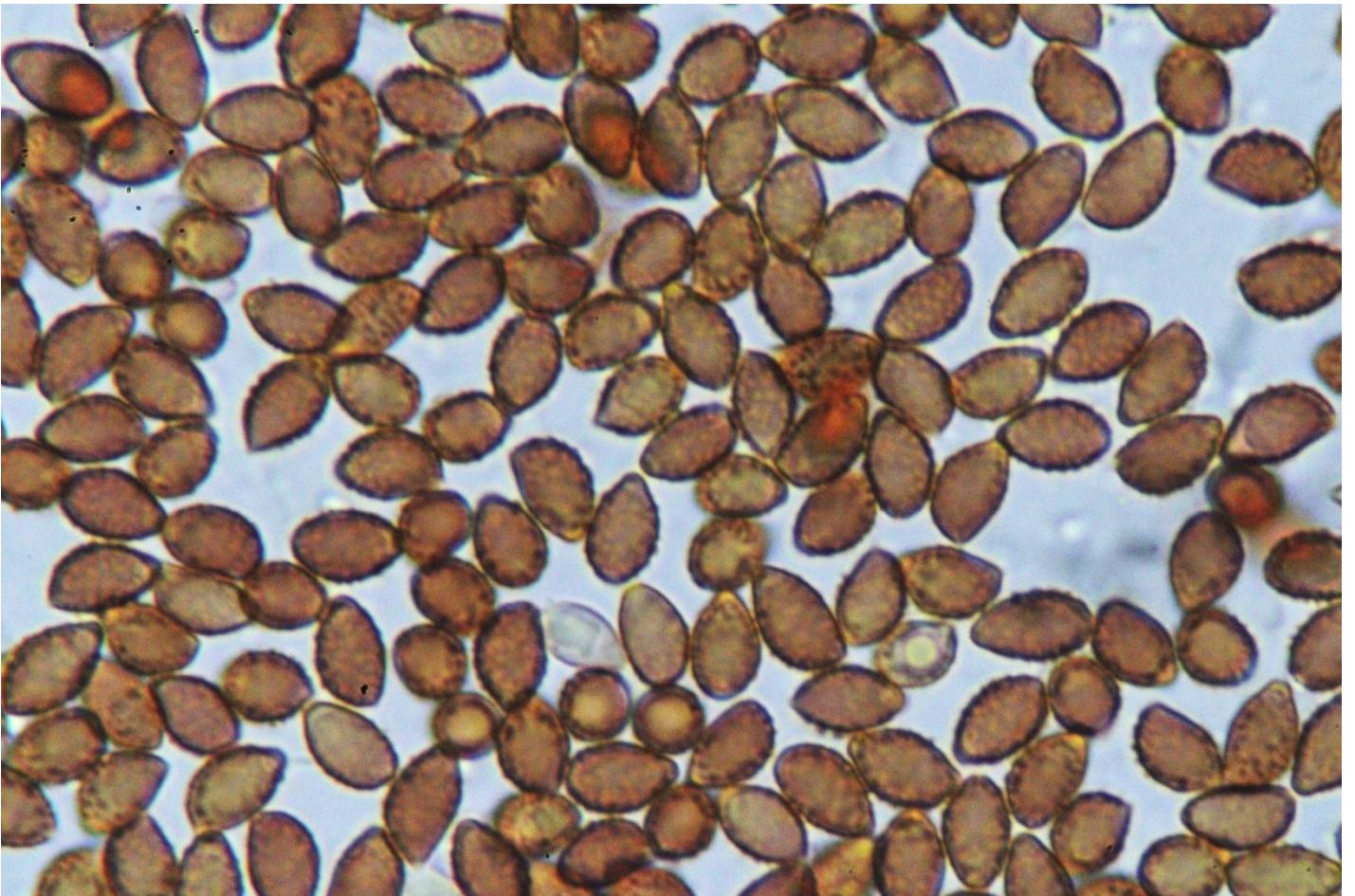
Cortinarius olivellus Rob. Henry



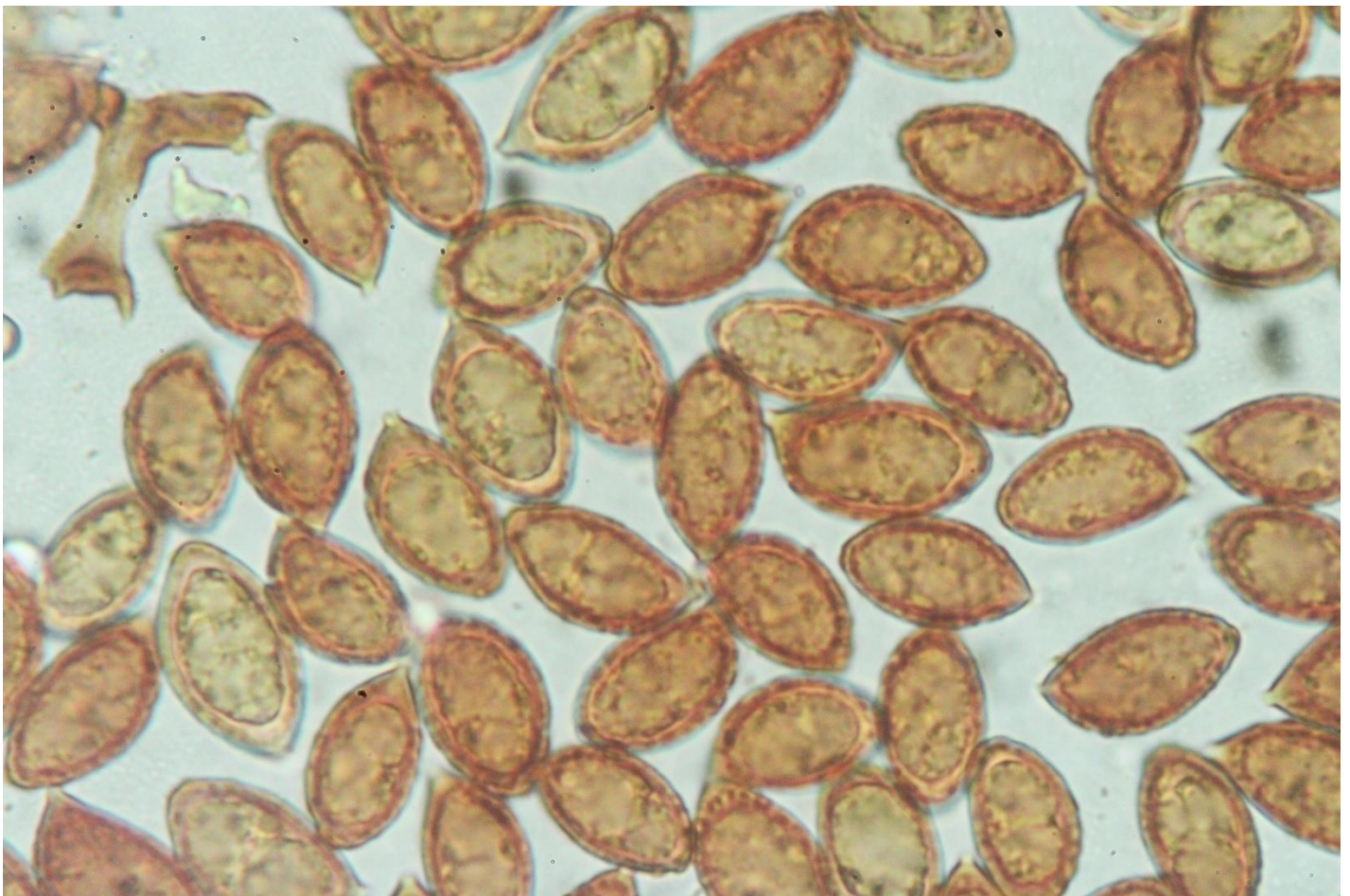
Cortinarius orellanus Fr.



NCS S 6020-y30r



Cortinarius palazonianus Vila, A. Ortega & Fern.-Brime



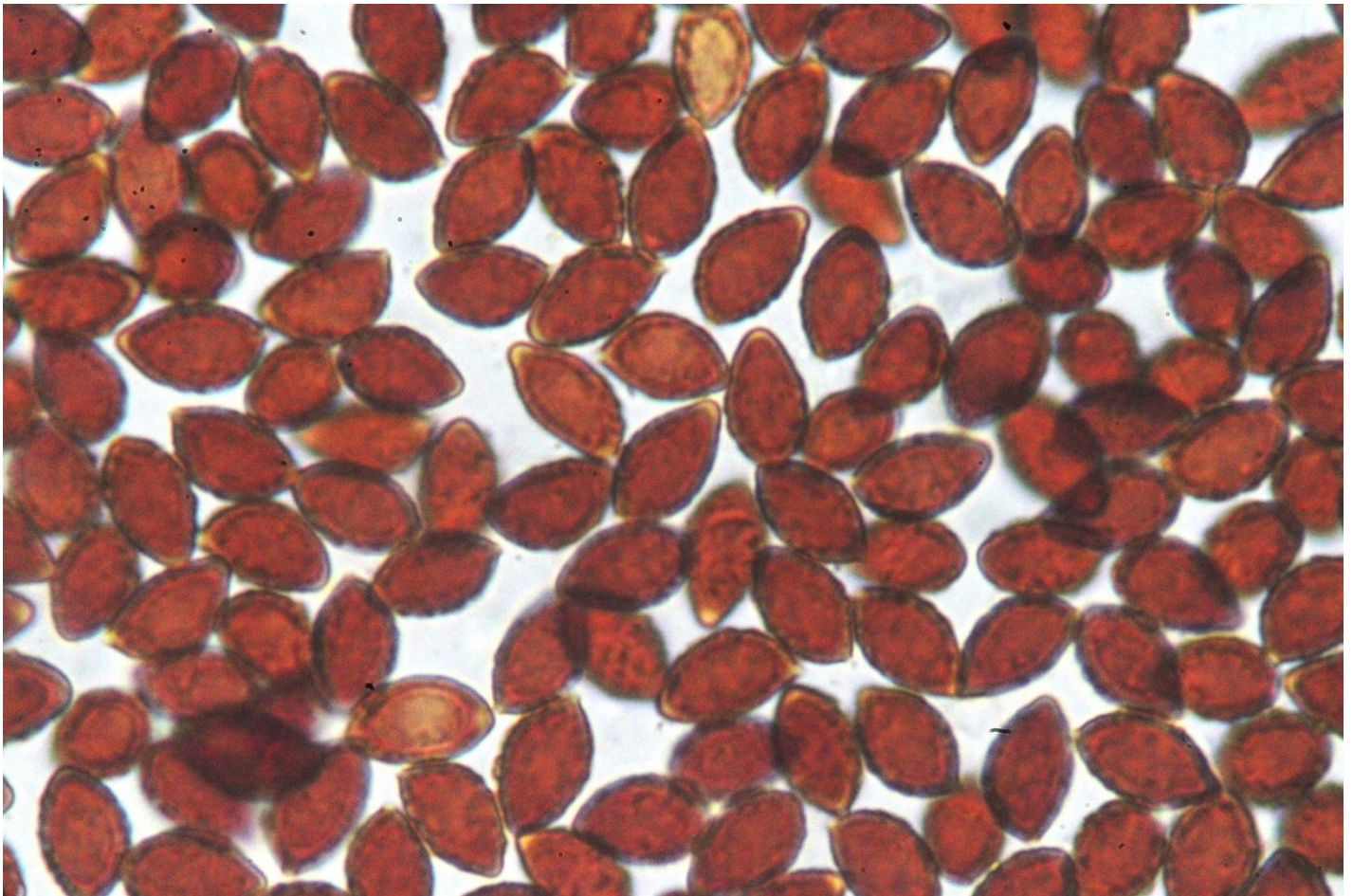
Cortinarius praestans (Cordier) Gillet



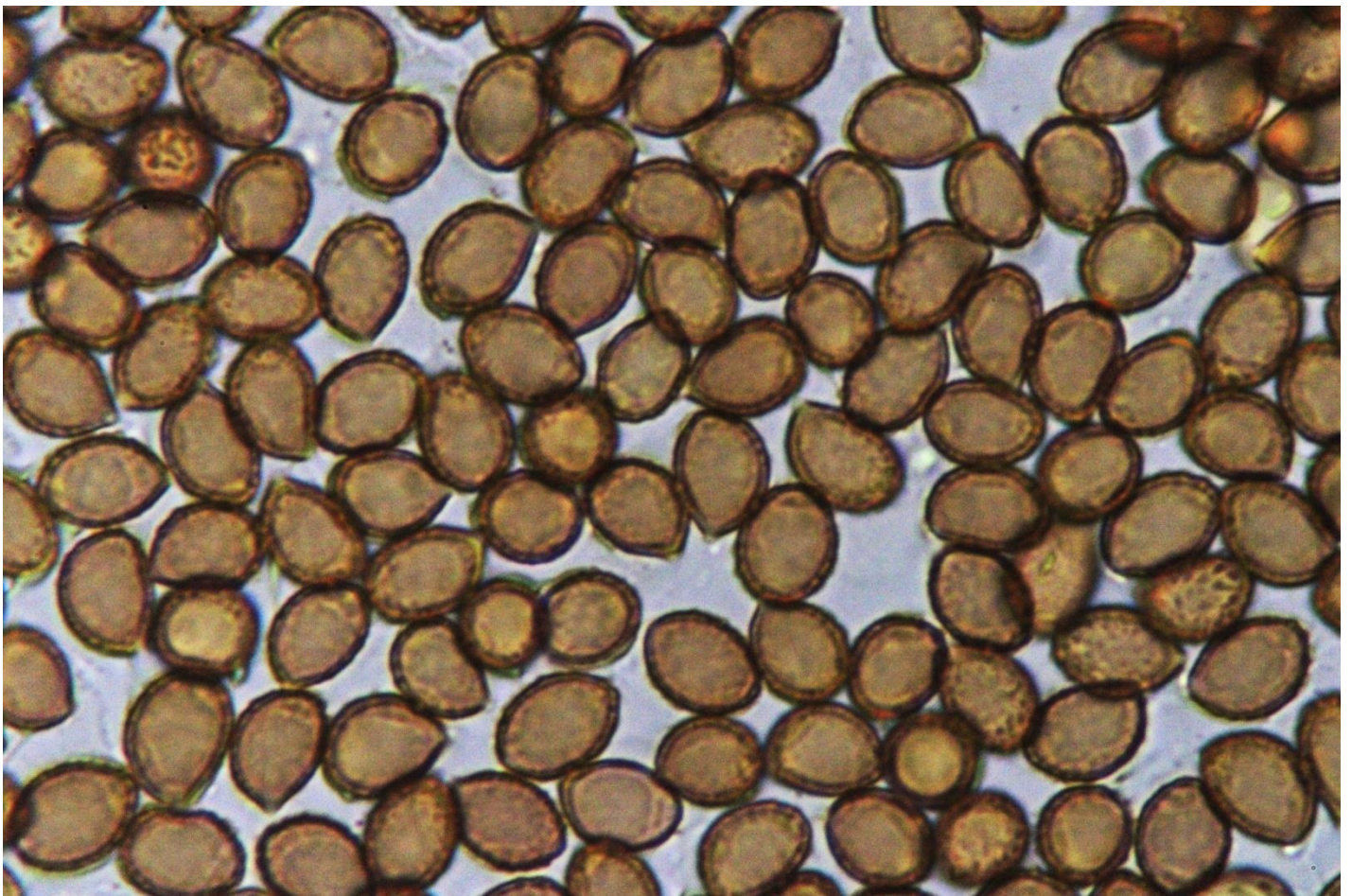
Cortinarius rapaceoides Bidaud, G. Rioussset & Rioussset



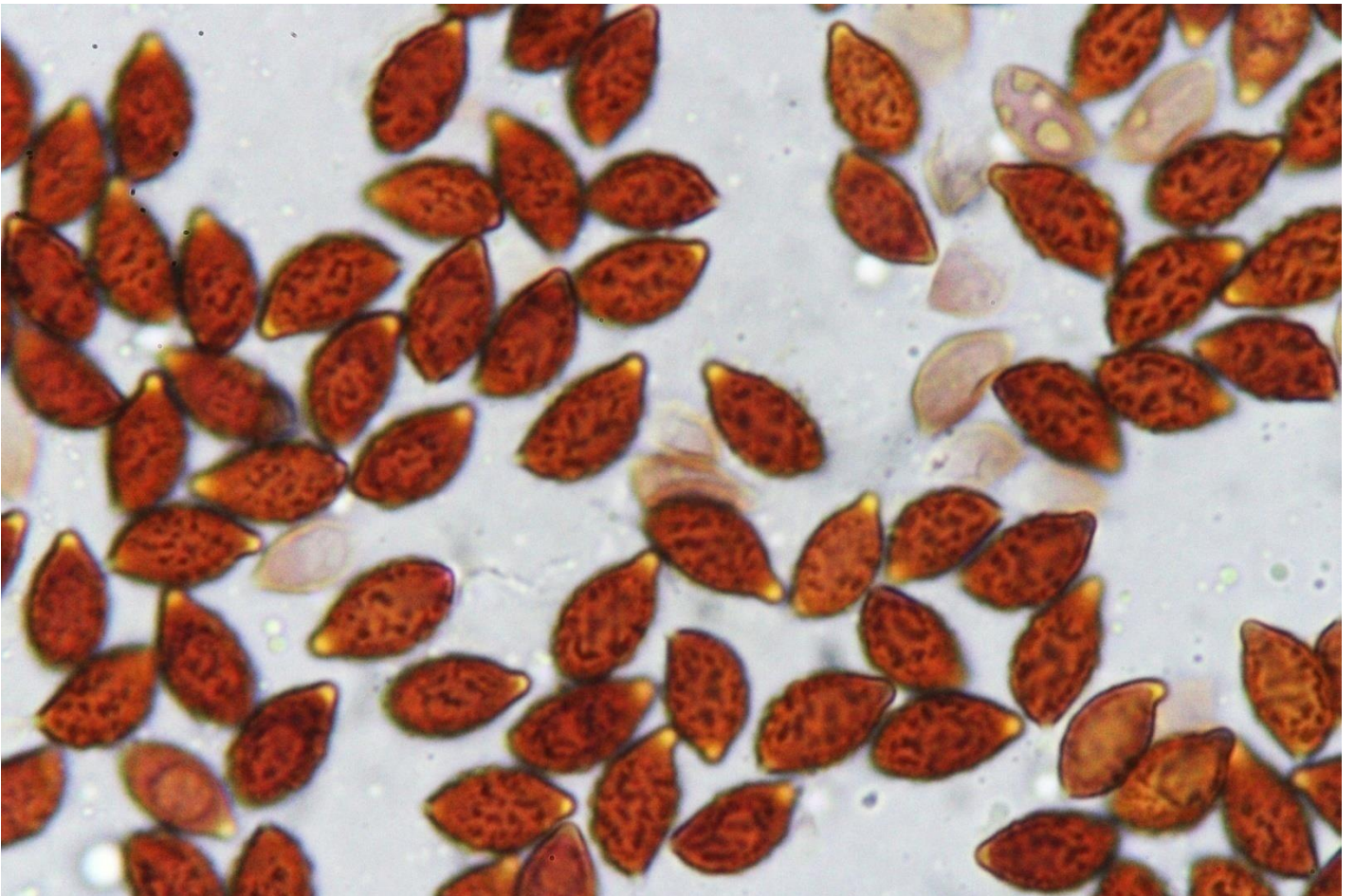
NCS S 3560-y80r



Cortinarius rapaceotomentosus Delaporte & Eyssart.



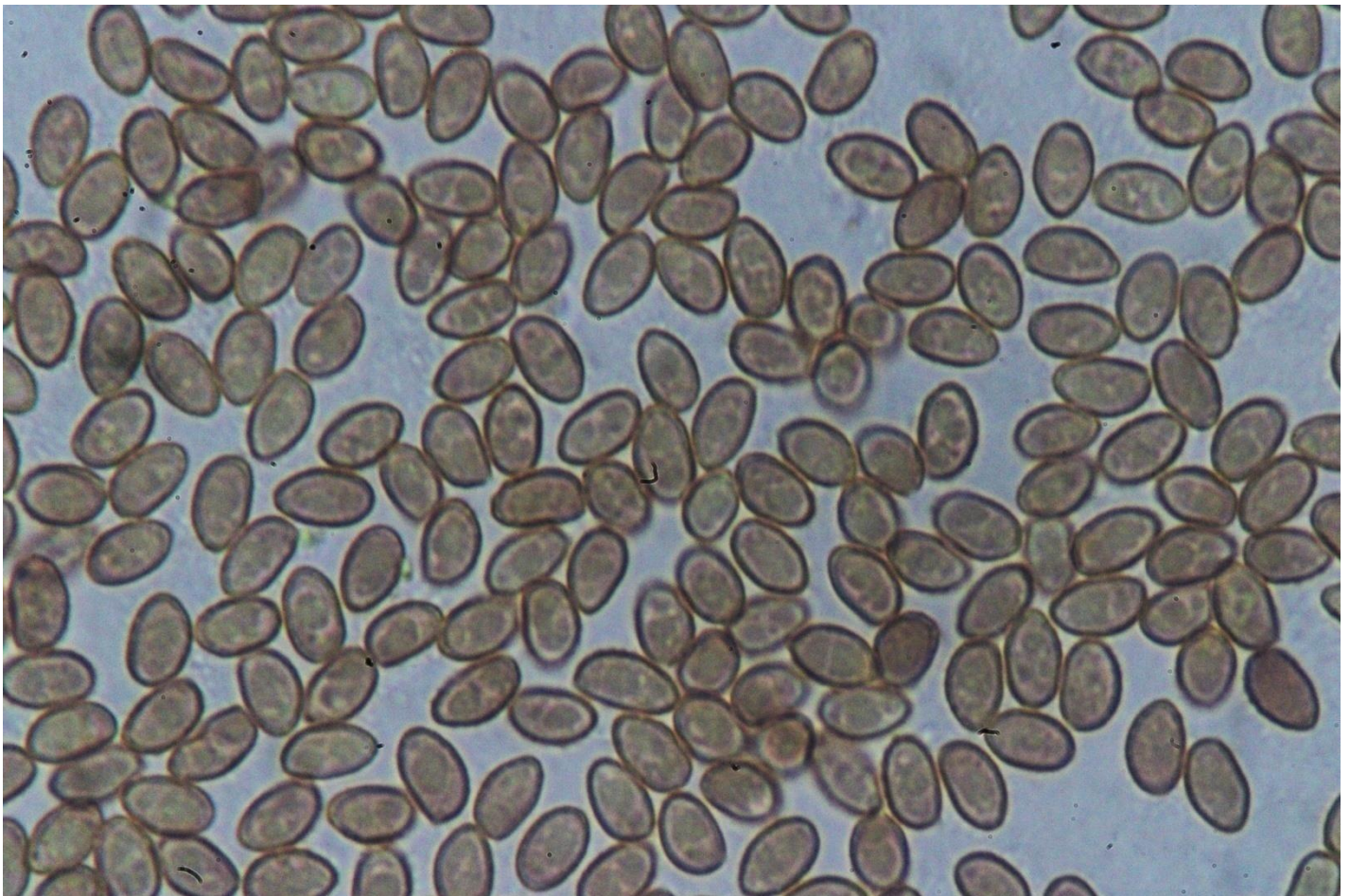
Cortinarius rubellus Cooke



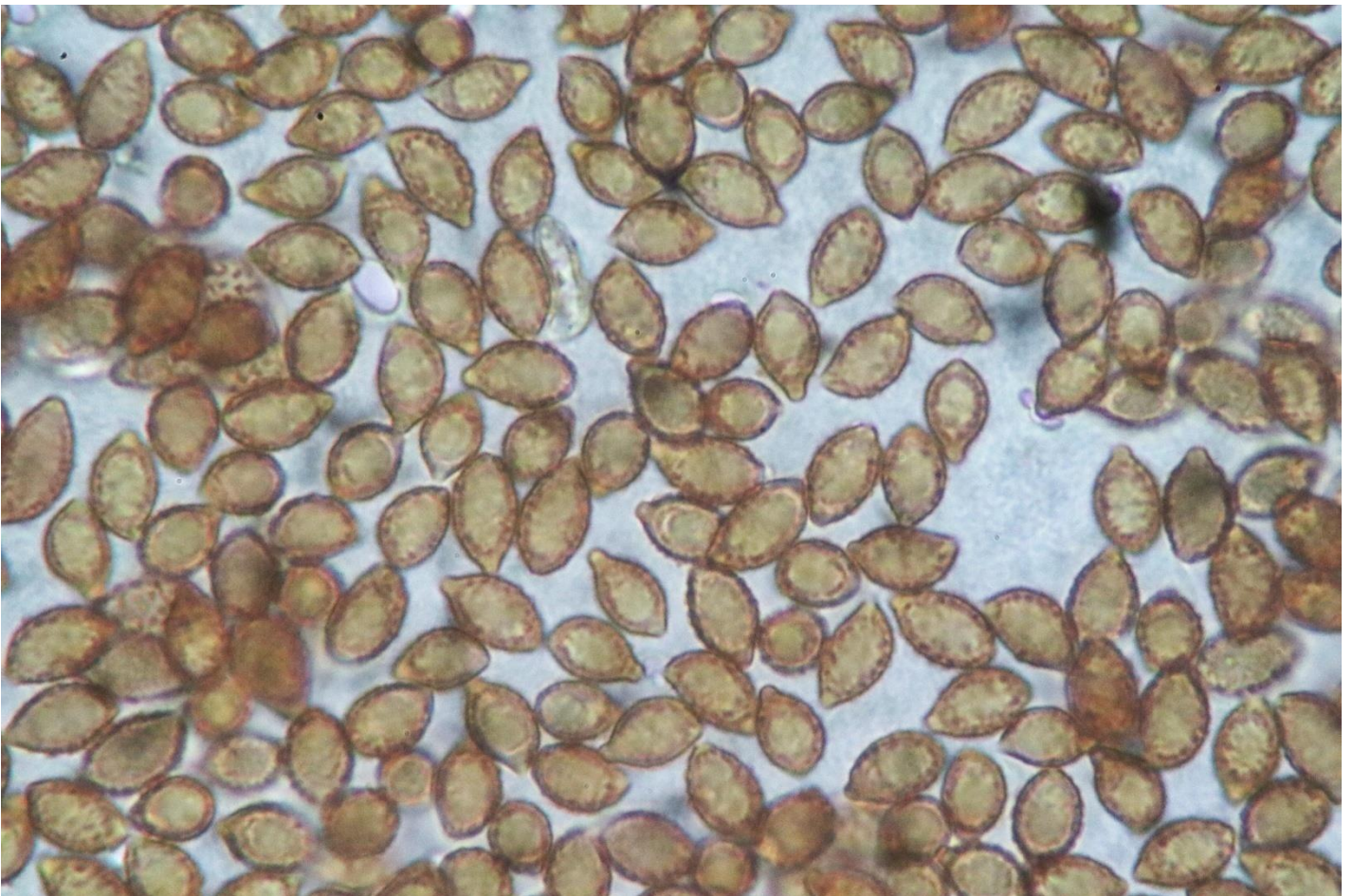
Cortinarius rufo-olivaceus (Pers.) Zaw.



NCS S 6005-y20r



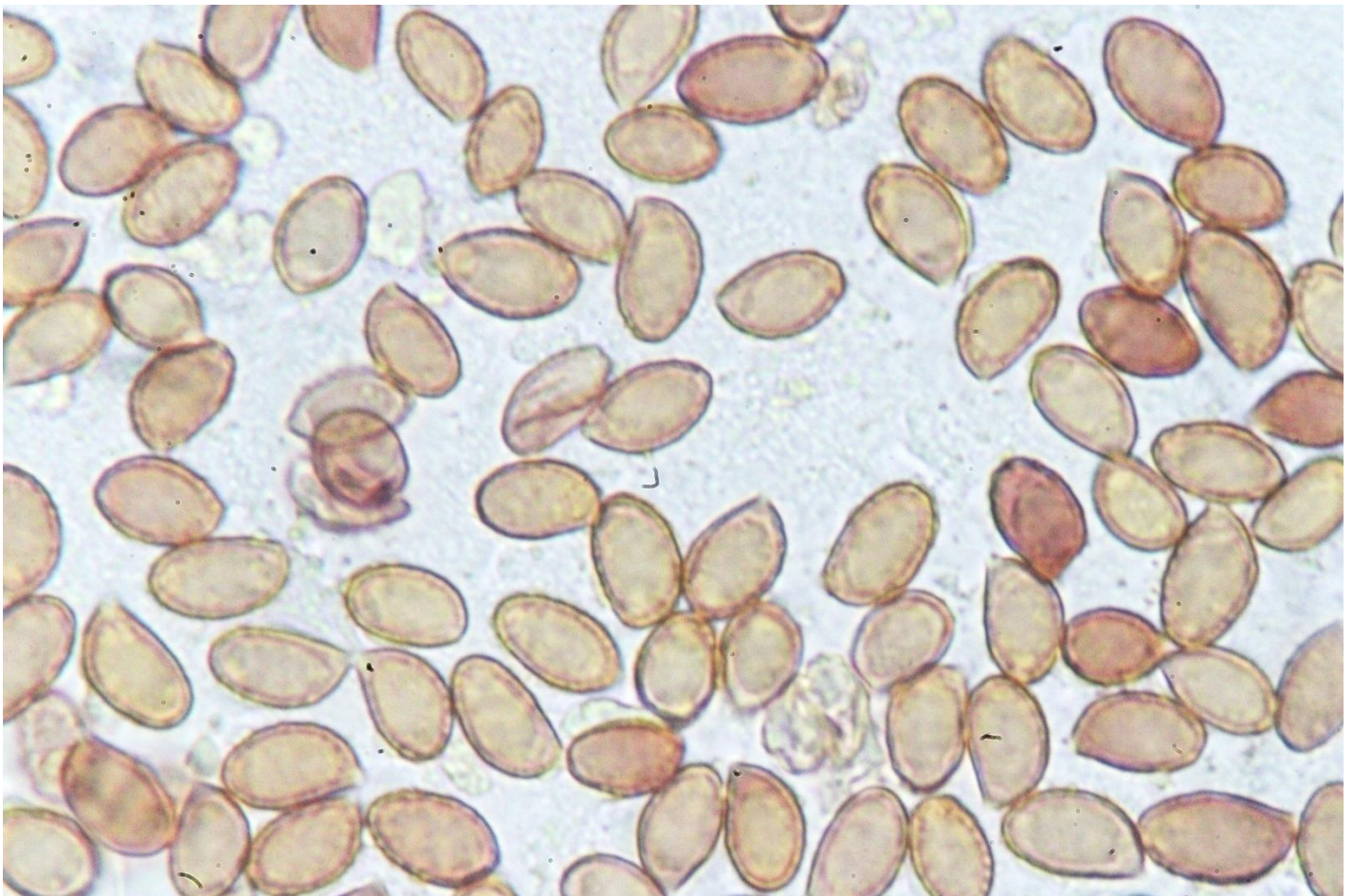
Cortinarius sanguineus (Wulfen) Gray



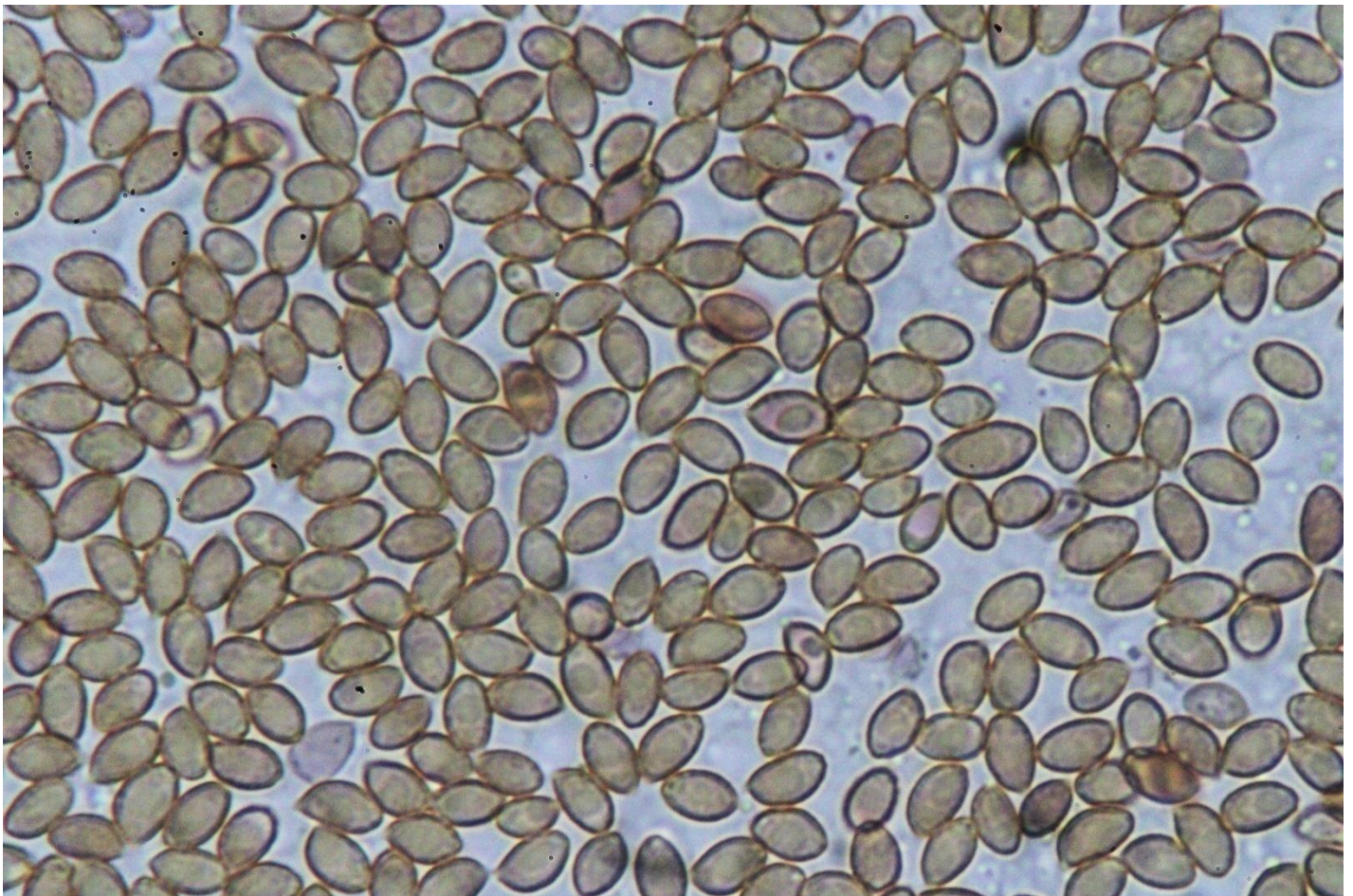
Cortinarius saporatus Britzelm.



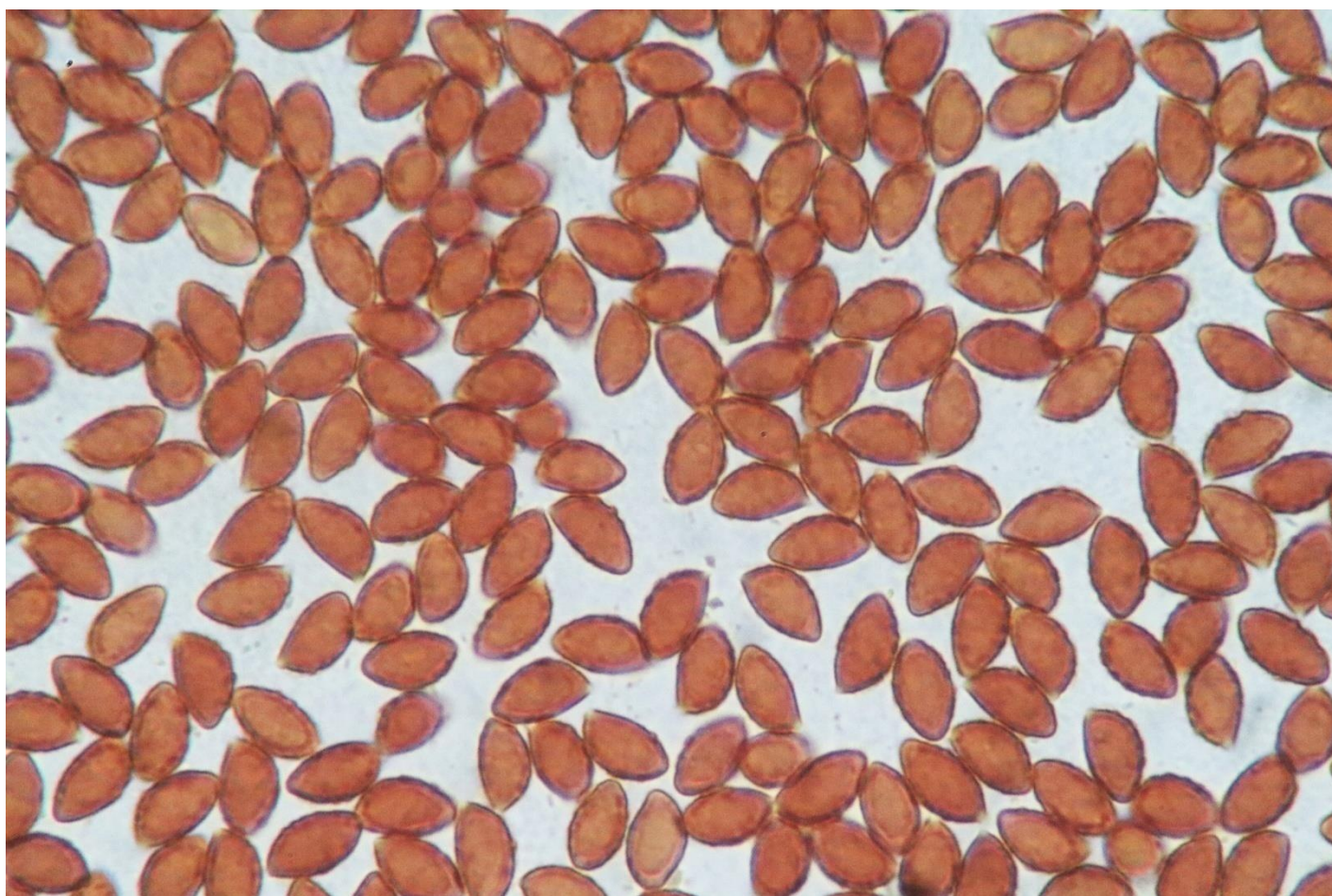
NCS S 4030-y90r



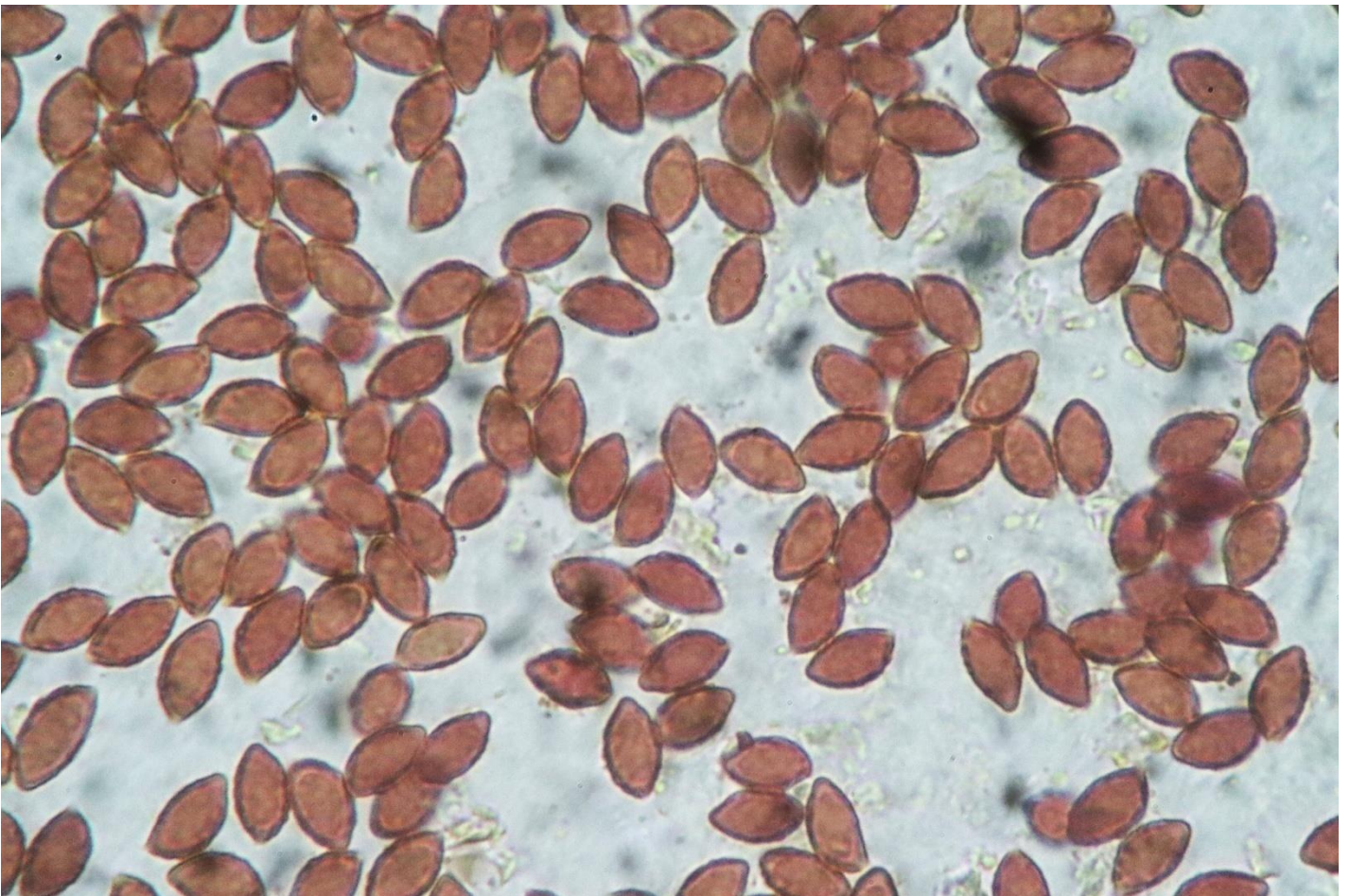
Cortinarius scaurus (Fr.) Fr.



Cortinarius semisanguineus (Fr.) Gillet



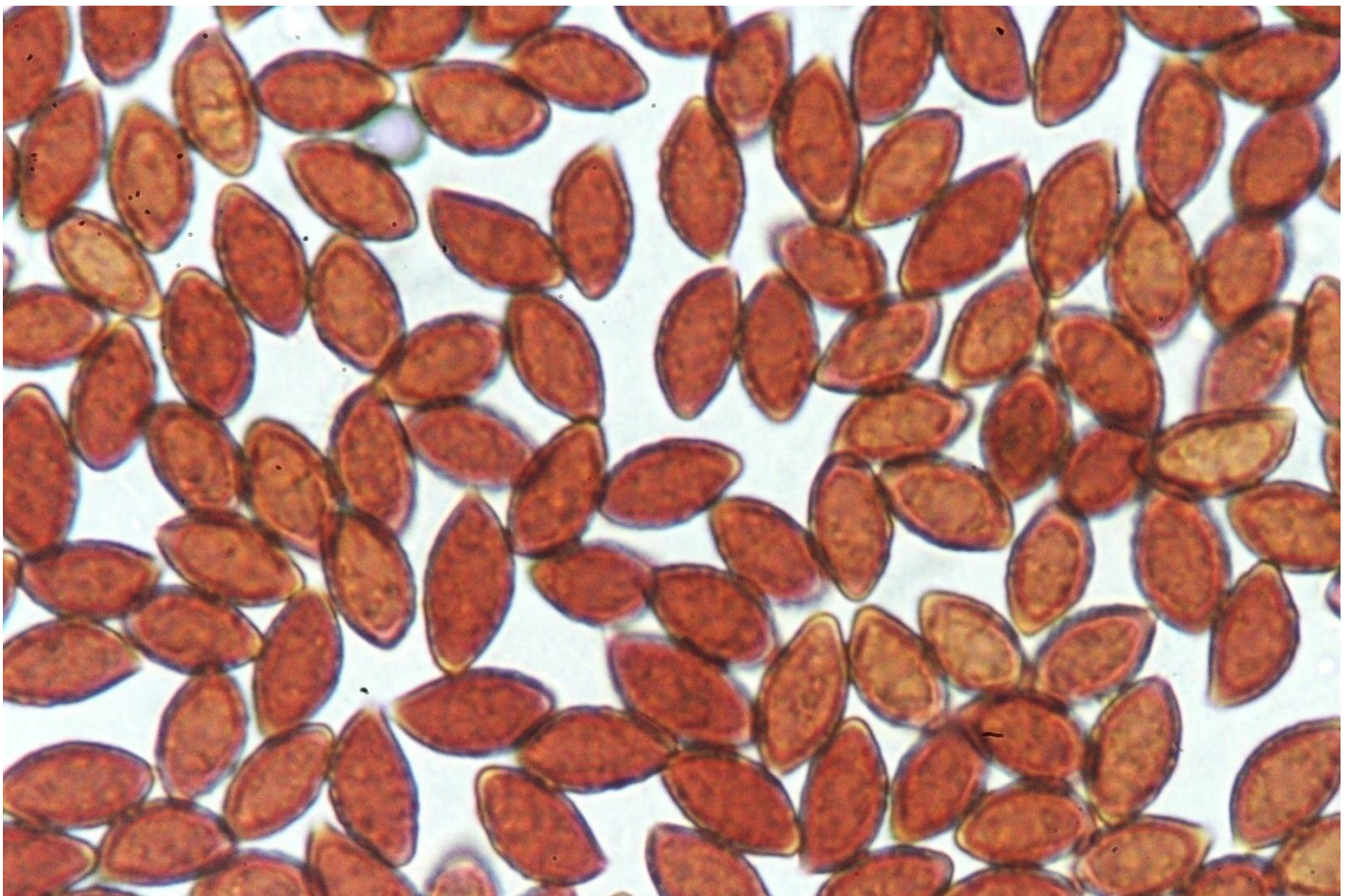
Cortinarius sodagnitus Rob. Henry



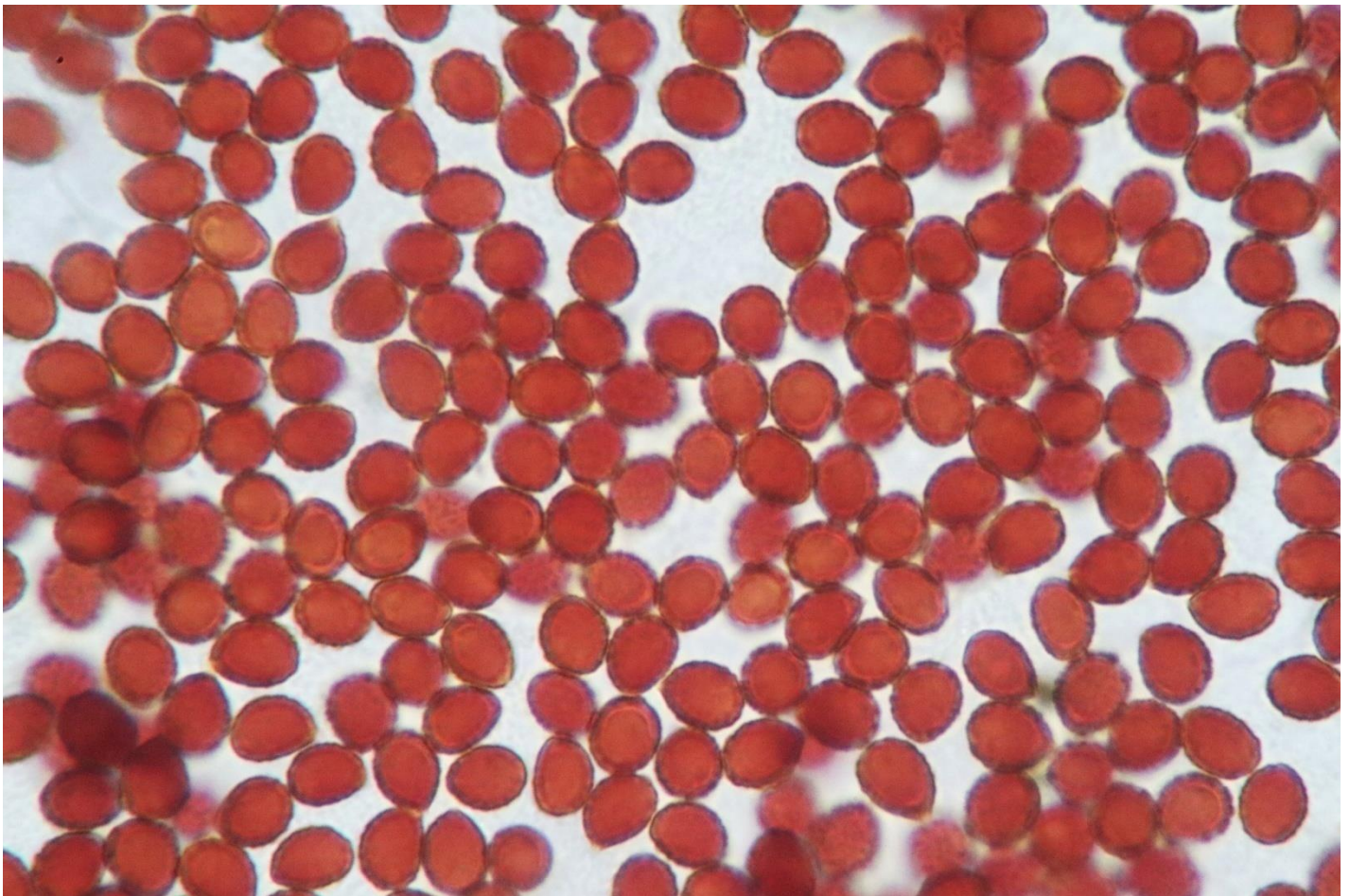
Cortinarius splendens Rob. Henry



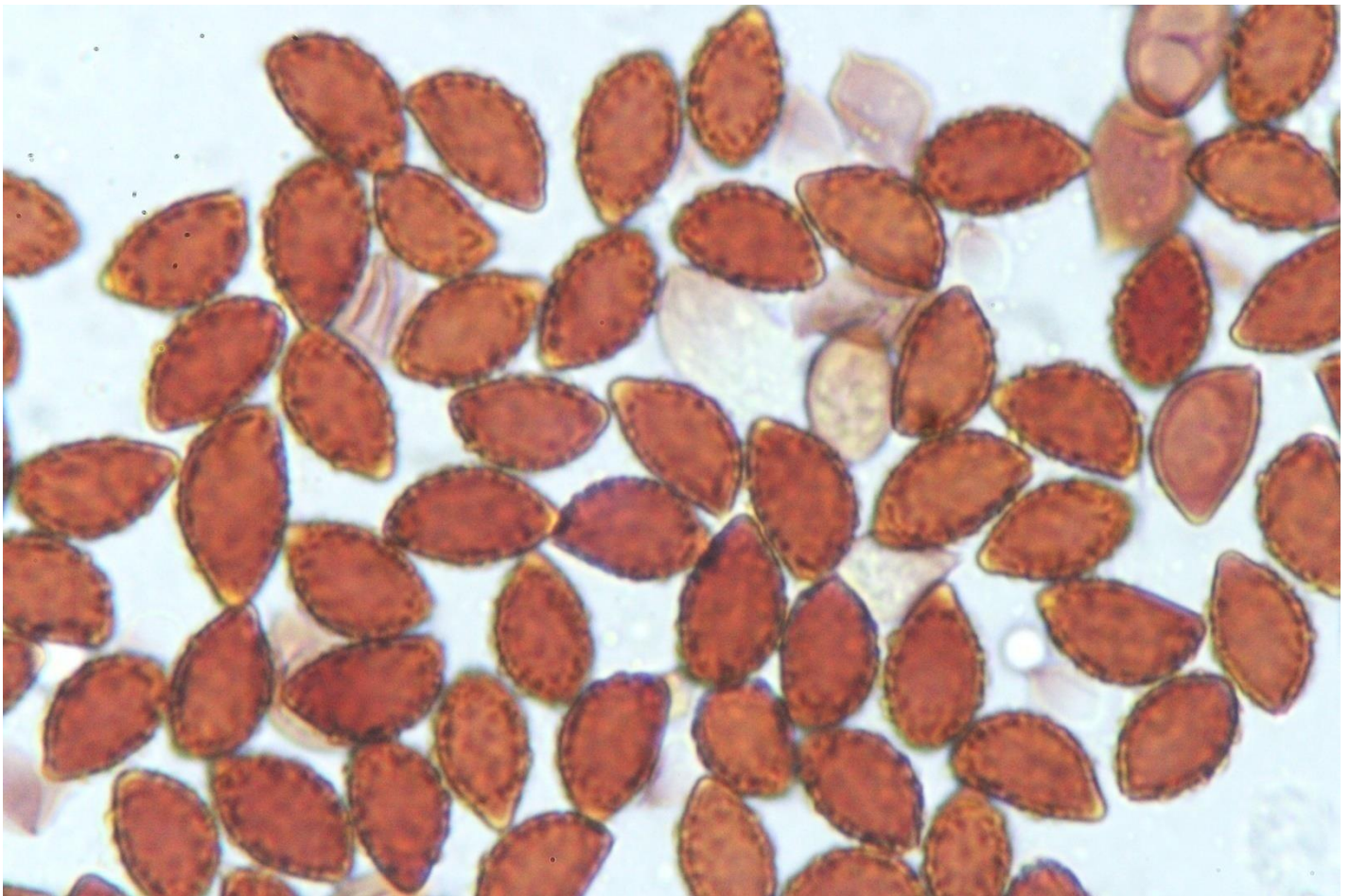
NCS S 3060-y70r



Cortinarius suaveolens Bataille & Joachim



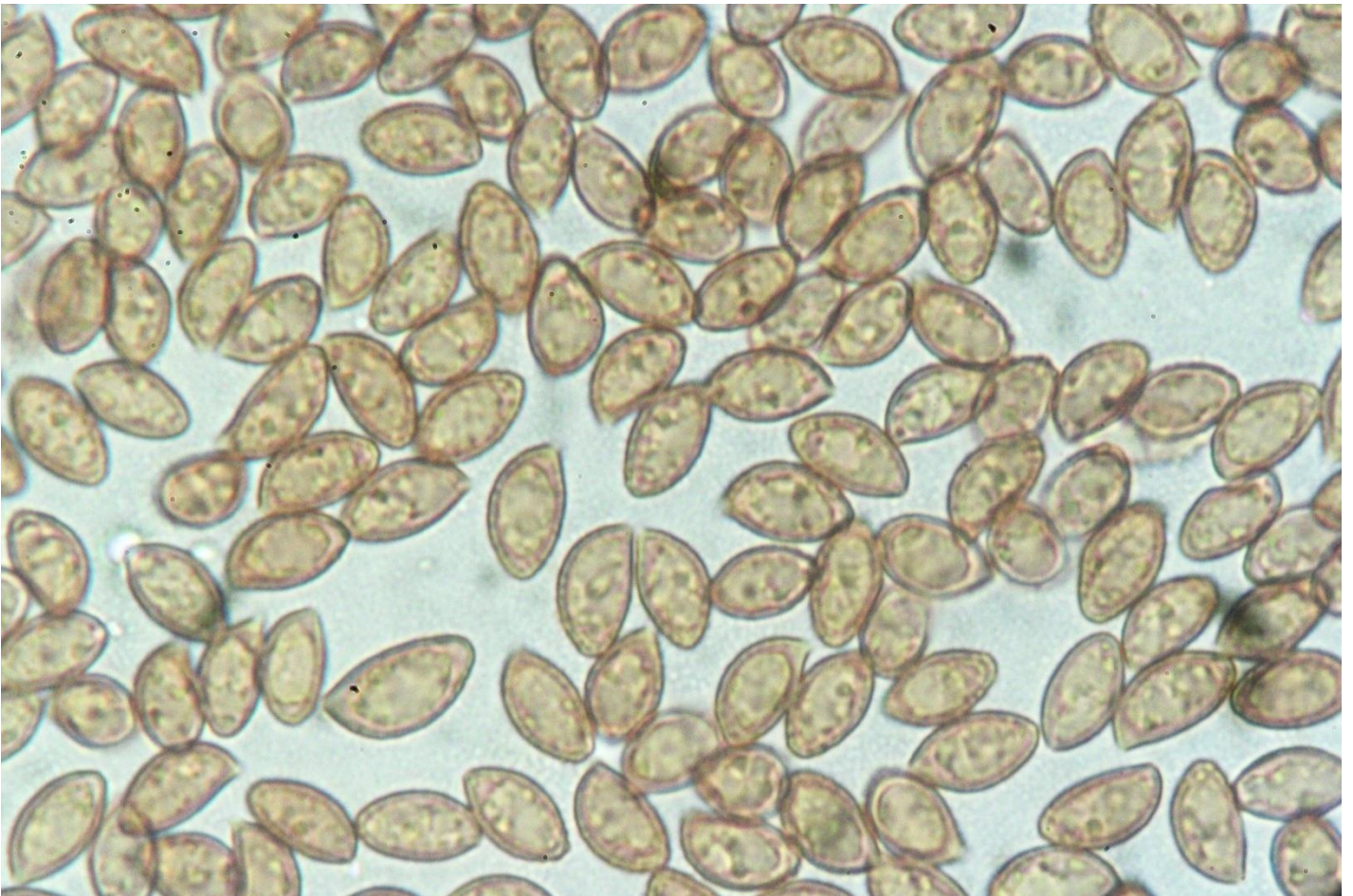
Cortinarius subcotoneus Bidaud



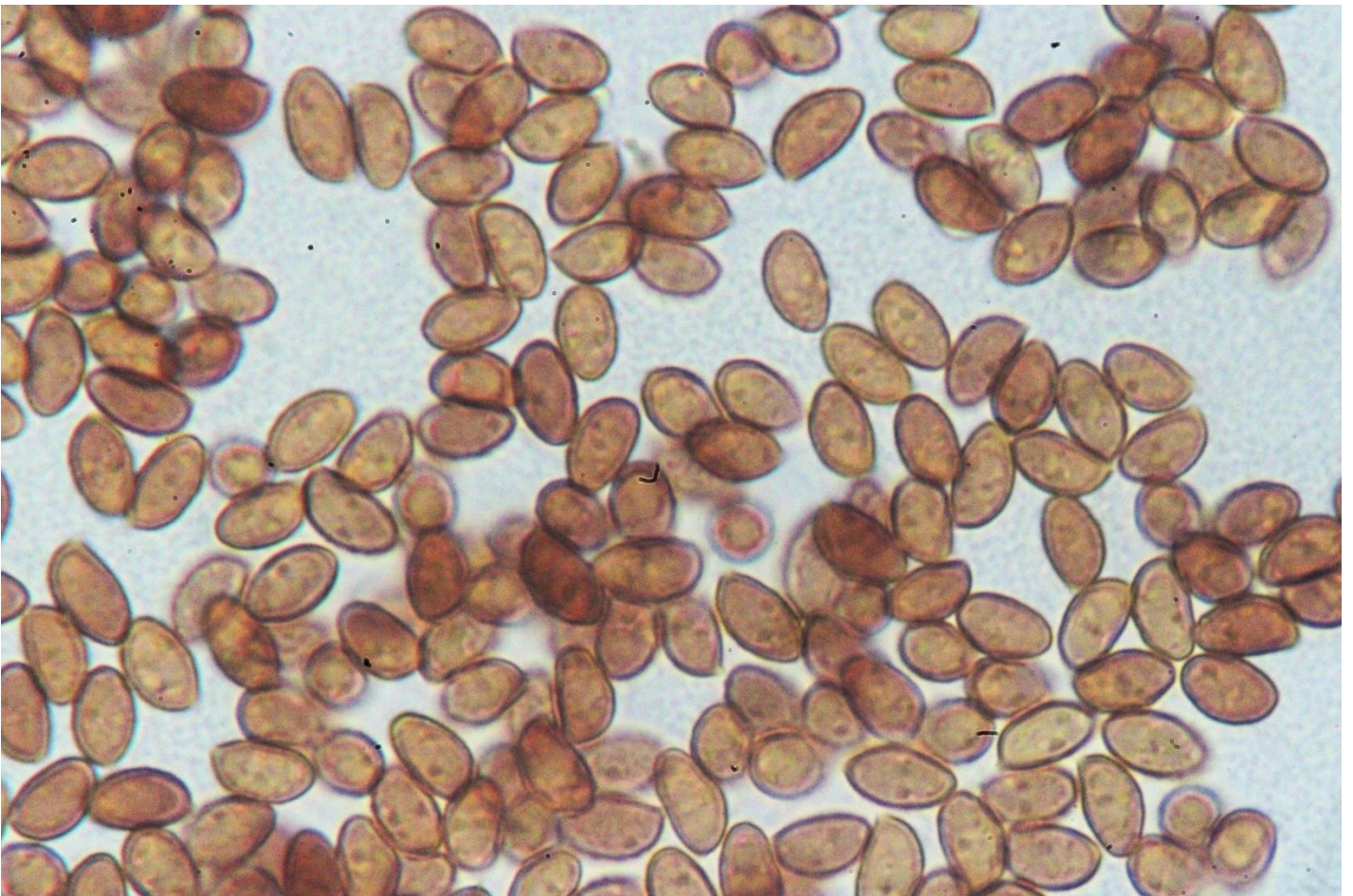
Cortinarius subelatorius Bidaud, Moënne-Locc. & Reumaux



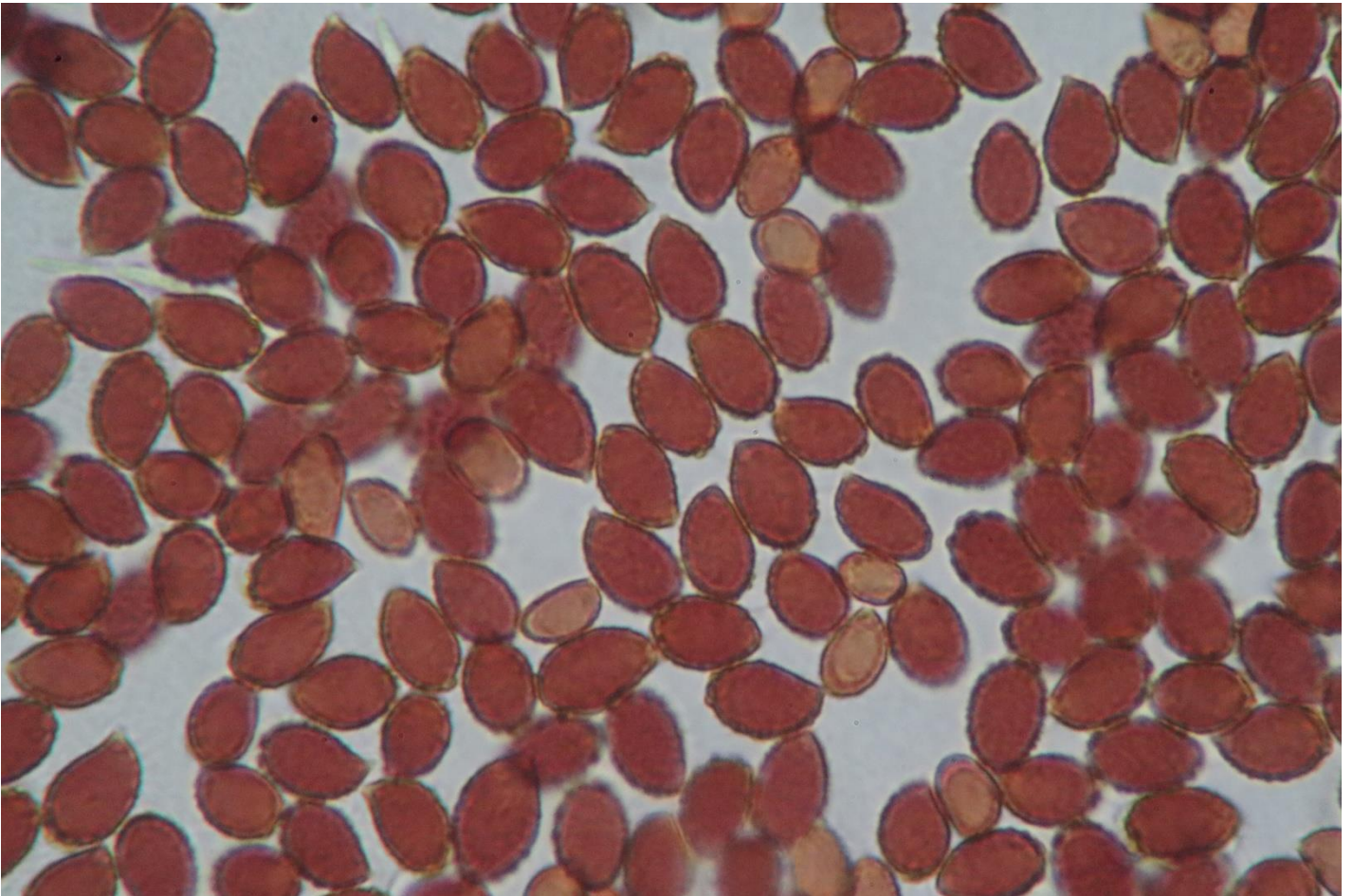
NCS S 2020-g90y



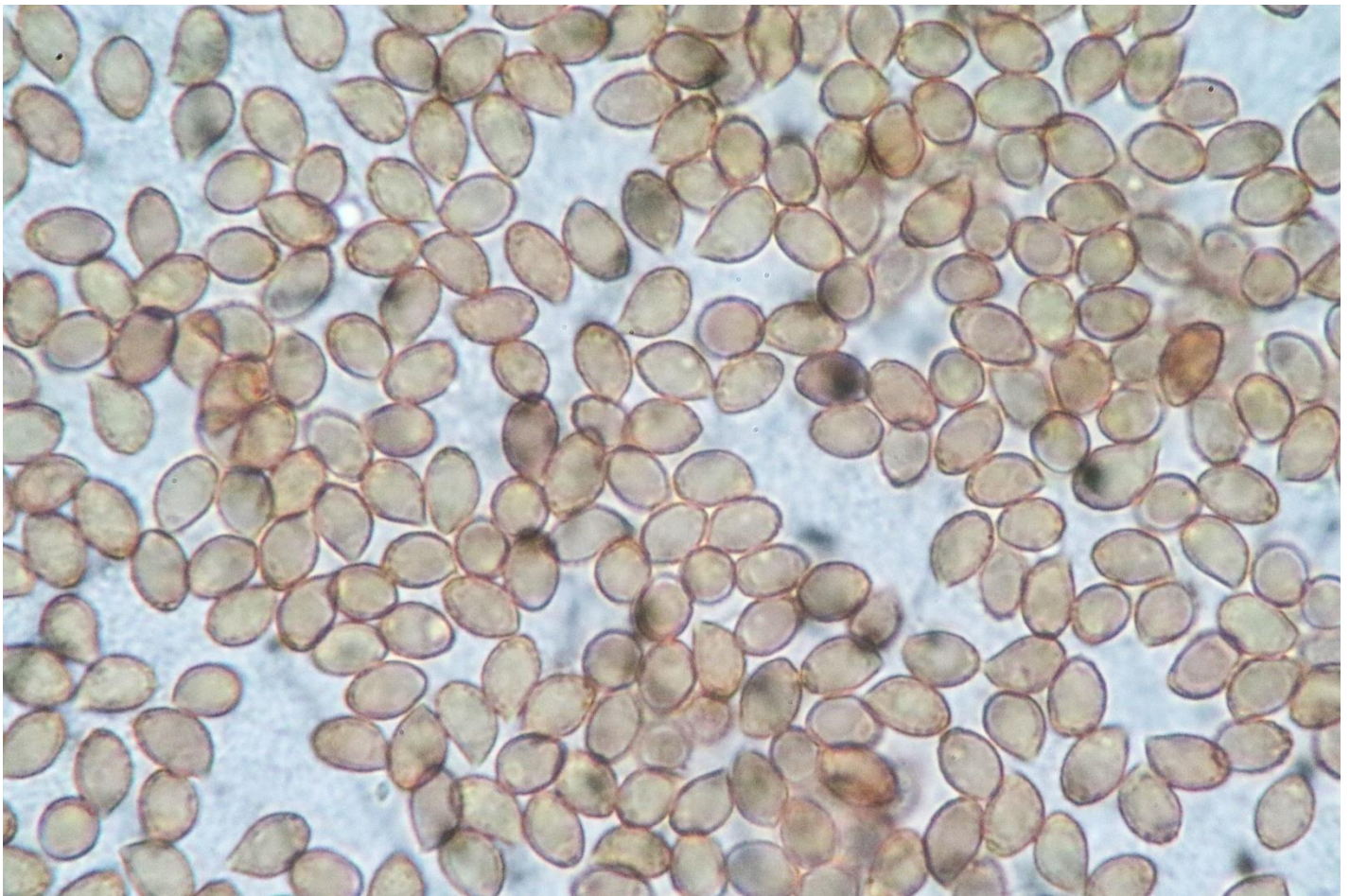
Cortinarius subvalidus Rob. Henry



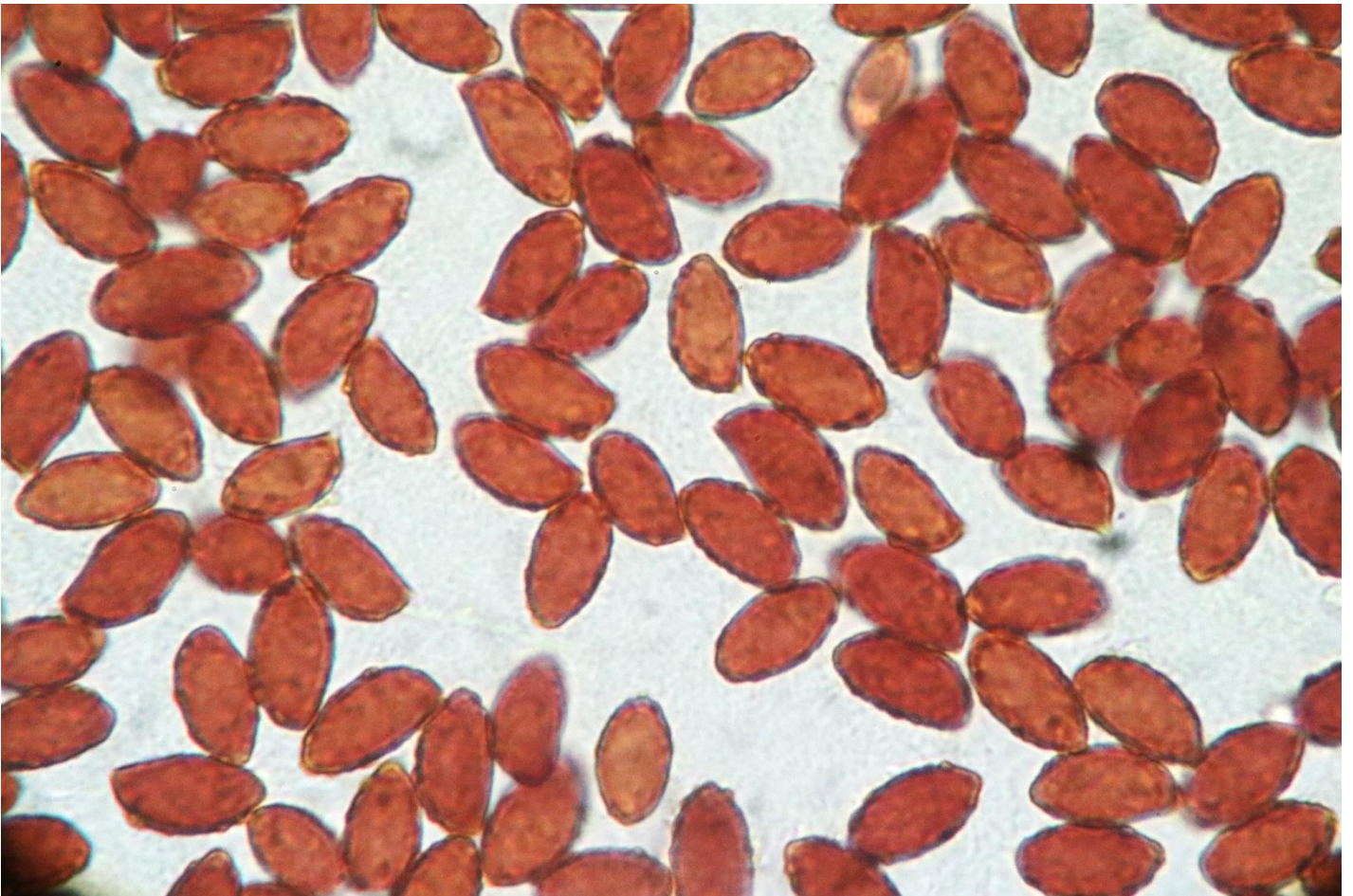
Cortinarius talus Fr.



Cortinarius torvus (Fr.) Fr.



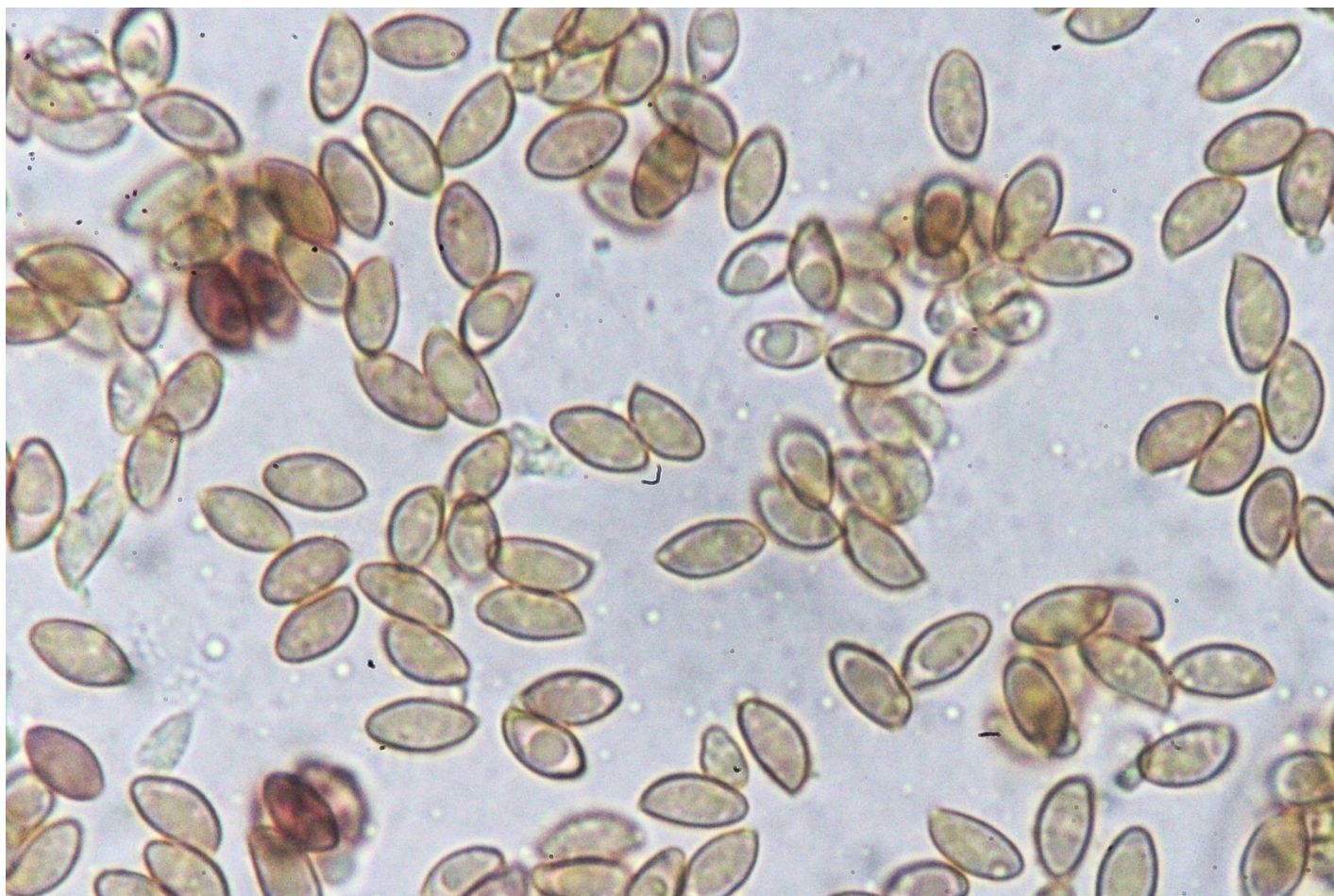
Cortinarius traganus (Fr.) Fr.



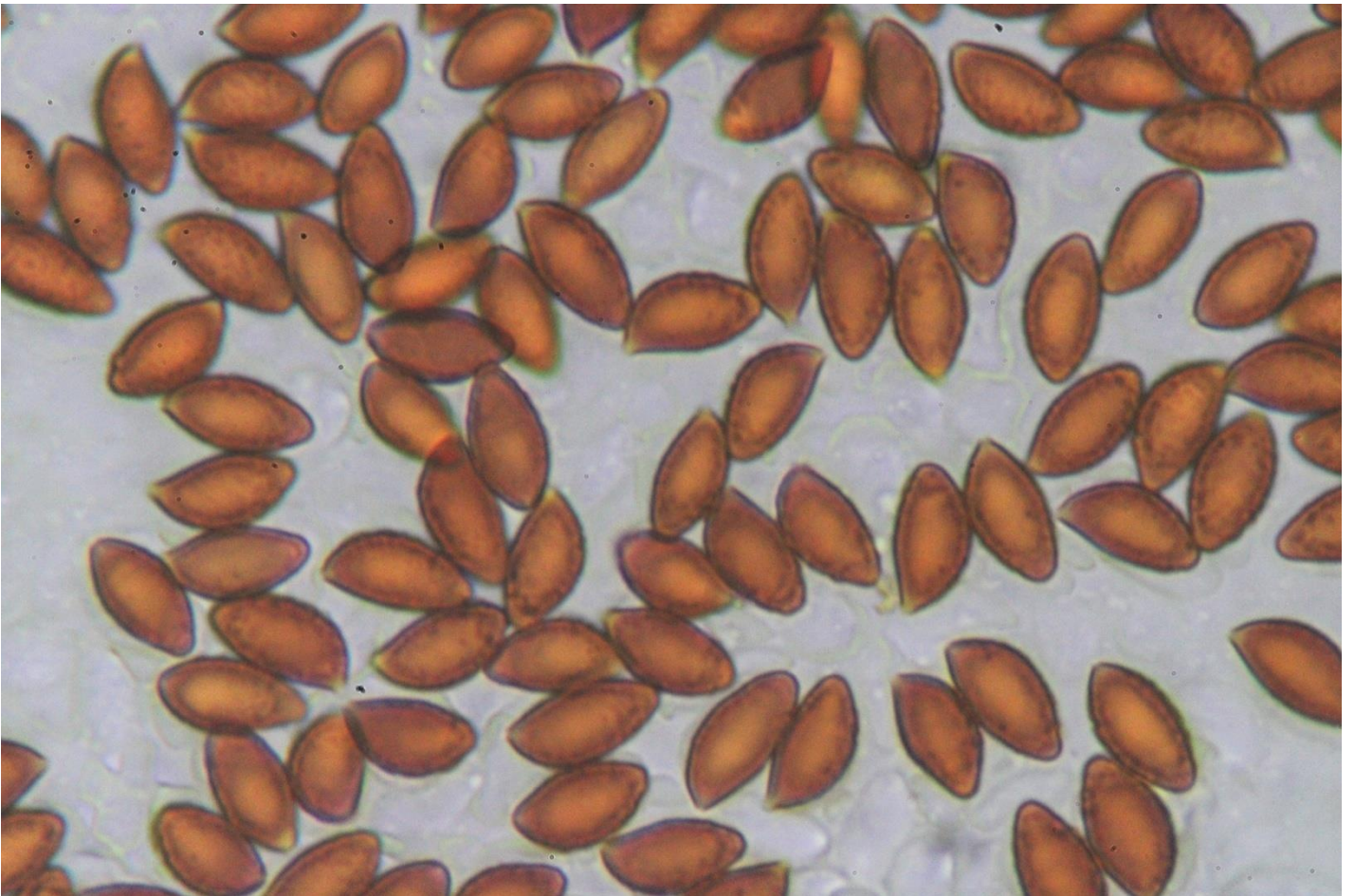
Cortinarius trivialis J.E. Lange



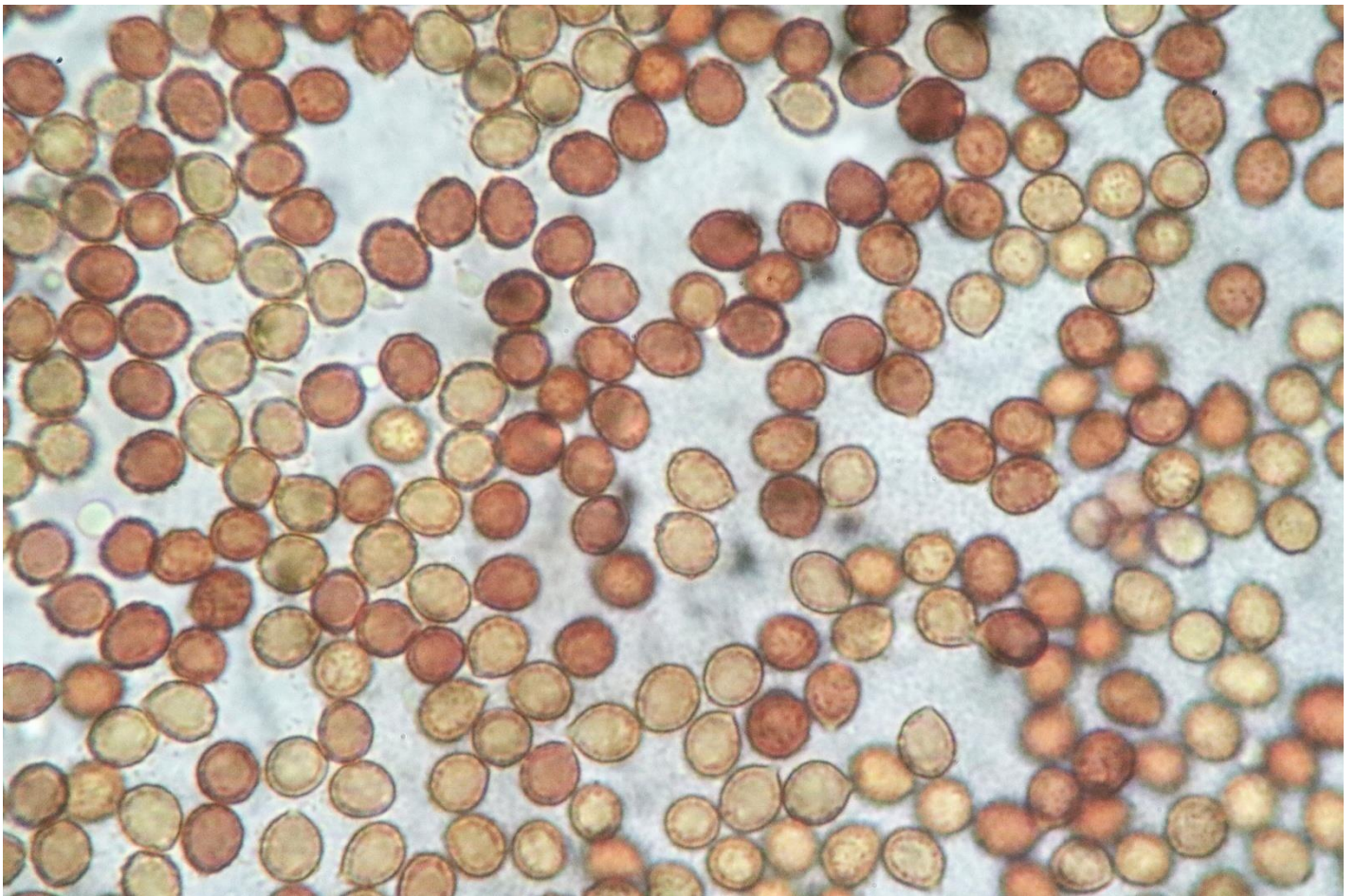
NCS S 3010-y



Cortinarius turmalis Fr.



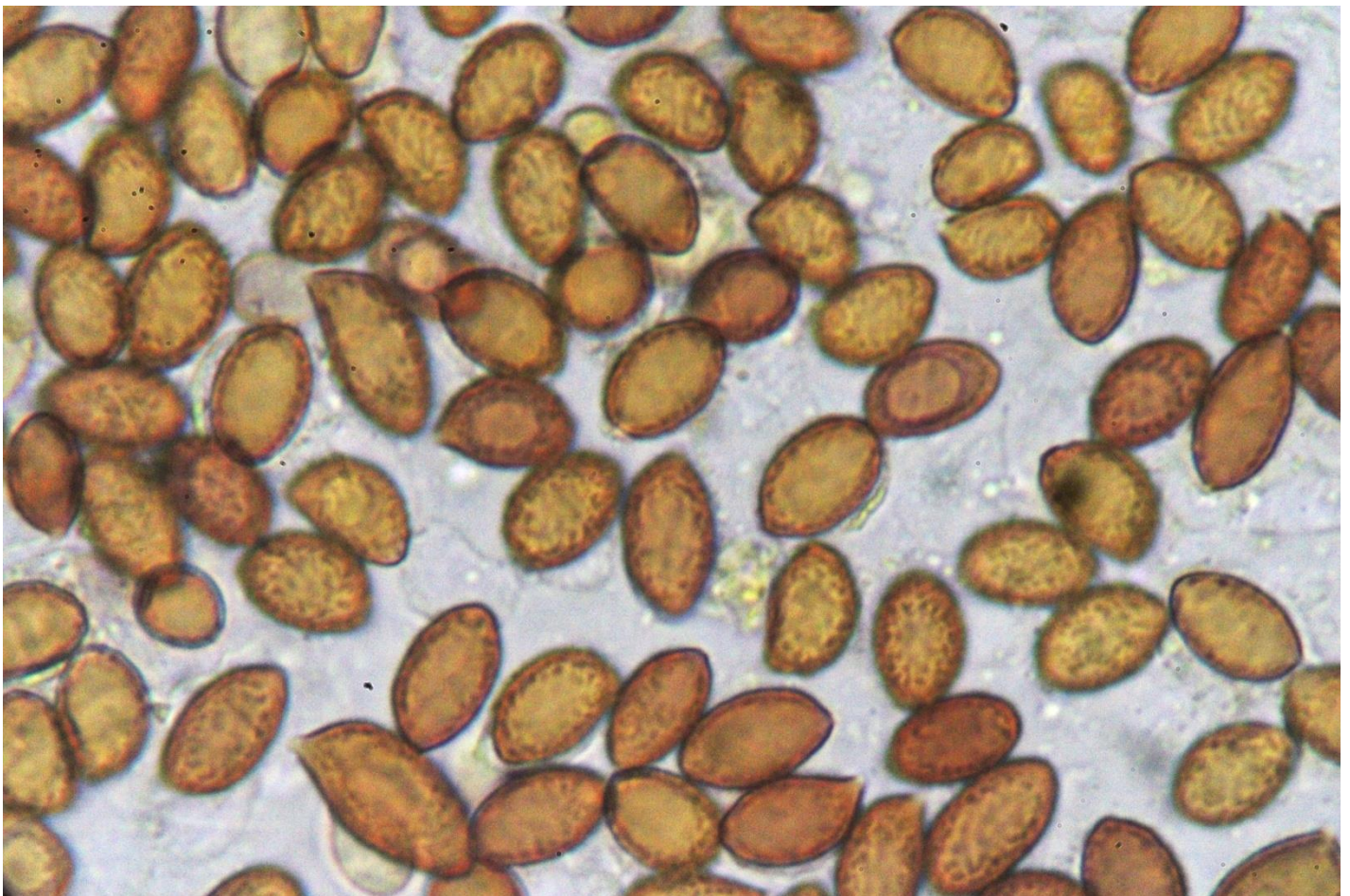
Cortinarius variegatus (Pers.) Fr.



Cortinarius venetus (Fr.) Fr.



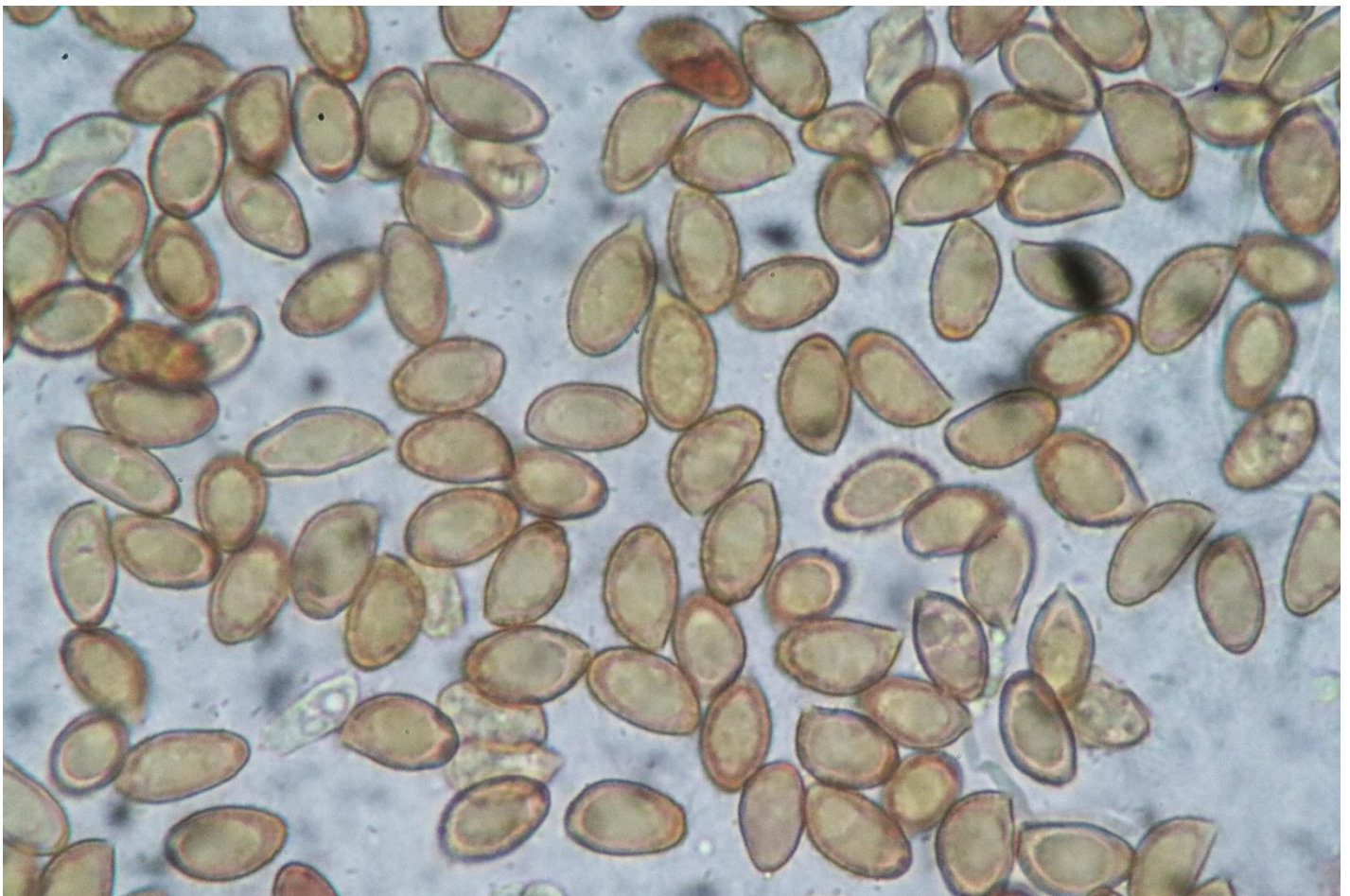
NCS S 4040-y20r



Cortinarius violaceus (L.) Gray



NCS S 4020-y



Cortinarius vulpinus (Velen.) Rob. Henry

Article received 23 March 2026, accepted 19 April 2026

Novelties in Family *Psathyrellaceae*. Part IX

Pietro Voto

Via Garibaldi 173, I-45010 Villadose (RO), Italy; pietrovoto@libero.it; <https://orcid.org/0000-0003-1922-1324>

TAXONOMIC NOVELTIES

New combinations

Candolleomyces bisporus (Kits van Wav.) Voto, *comb. nov.* [MB 863561]

Basionym: ***Psathyrella typhae* var. *bispora*** Kits van Wav., *Persoonia* Suppl. 2: 282 (1985)

Candolleomyces lacuum (Huijsman) Voto, *comb. nov.* [MB 863562]

Basionym: ***Psathyrella lacuum*** Huijsman, *Fungus* 25: 39 (1955)

Candolleomyces pallidisporus (Dennis) Voto, *comb. nov.* [MB 863563]

Basionym: ***Psathyrella pallidispora*** Dennis, *Kew Bull., Addit. Ser.* 3: 466 (1970)

Candolleomyces patialensis (Harw. Kaur & M. Kaur) Voto, *comb. nov.* [MB 863564]

Basionym: ***Psathyrella patialensis*** Harw. Kaur & M. Kaur, in Harwinder, Malik & Munruchi, *Mushroom Research* 29(1): 15 (2020)

Candolleomyces radicellatus (Malençon ex Pacioni) Voto, *comb. nov.* [MB 863565]

Basionym: ***Psathyrella radicellata*** Malençon ex Pacioni, *Micol. Veg. Medit.* 2(2): 148 (1988) [1987]

Candolleomyces rawlae (Voto) Voto, *comb. nov.* [MB 863566]

Basionym: ***Psathyrella rawlae*** Voto, *Boll. Assoc. Micol. Ecol. Romana* 109(1): 13 (2020)

Candolleomyces varicosus (A. Pearson) Voto, *comb. nov.* [MB 863567]

Basionym: ***Psathyrella varicosa*** A. Pearson, *Trans. Br. mycol. Soc.* 33(3-4): 308 (1951) [1950]

Coprinopsis longipes (Peck) Voto, *comb. nov.* [MB 863568]

Basionym: ***Hypholoma longipes*** Peck, *Bull. Torrey bot. Club* 22: 204 (1895)

SYNONYMIES PROPOSED

Psathyrella fragilissima (Kauffman) A.H. Sm.

synonym of ***Coprinopsis pseudomarcescibilis*** Heykoop, G. Moreno & P. Alvarado

Psathyrella pseudolongipes A.H. Sm.

synonym of ***Psathyrella fusca*** (J.E. Lange) A. Pearson

Article received 19 January 2026, accepted 20 April 2026

***Hysteropeltella moravica* (Ascomycota, Dothideales) in Bosnia**

Dusko Trivič

trivicdusko682@gmail.com

Key words:

Pezizomycotina

Dothideomycetes

Dothideomycetidae

Abstract: Based on a morphological study, a collection of *Hysteropeltella moravica* is described from Bosnia and Herzegovina on *Thuja* branches in a moist environ. This finding expands its diffusion to the Balkans and its growth substratum to plants of *Thuja*.

INTRODUCTION

The genus *Hysteropeltella* Petr. was established by Petrak (1923) to accommodate the species *H. moravica* Petr. and since then it has remained a monospecific genus. Its distinguishing characters among the fungi informally and classically called Discomycetes are elongate apothecial ascomata; broadly oblong to ellipsoidal or clavate asci with an amyloid apex; and uniseptate, clavate-oblong to fusoid or ellipsoidal ascospores. Its placement in *Dothideomycetes* was first proposed by Lumbsch and Huhndorf (2010).

Based on information extracted from the website <https://dothideomycetes.org/>, *Hysteropeltella* is currently, though pending molecular conformation, included in the family *Patellariaceae* Corda, as proposed by Yacharoen, Tian, Chomnunti *et al.* (2015), while in a previous study by Ariyawansa *et al.* (2013) it had been placed in *Schizothyriaceae* Höhn. ex Trotter [as '*Schizothyrieae*'].

To date, no collection attributed to it has ever been sequenced.

MATERIALS AND METHODS

Basidiocarps were photographed in the field using Canon Ixus 185 and Canon Ixus 285 HS cameras. Microscopy data and images were obtained from fresh material observed in Melzer's solution.



BRIEF DESCRIPTION

Hysteropeltella moravica Petr.

Annales Mycologici 21(1-2):10 (1923)

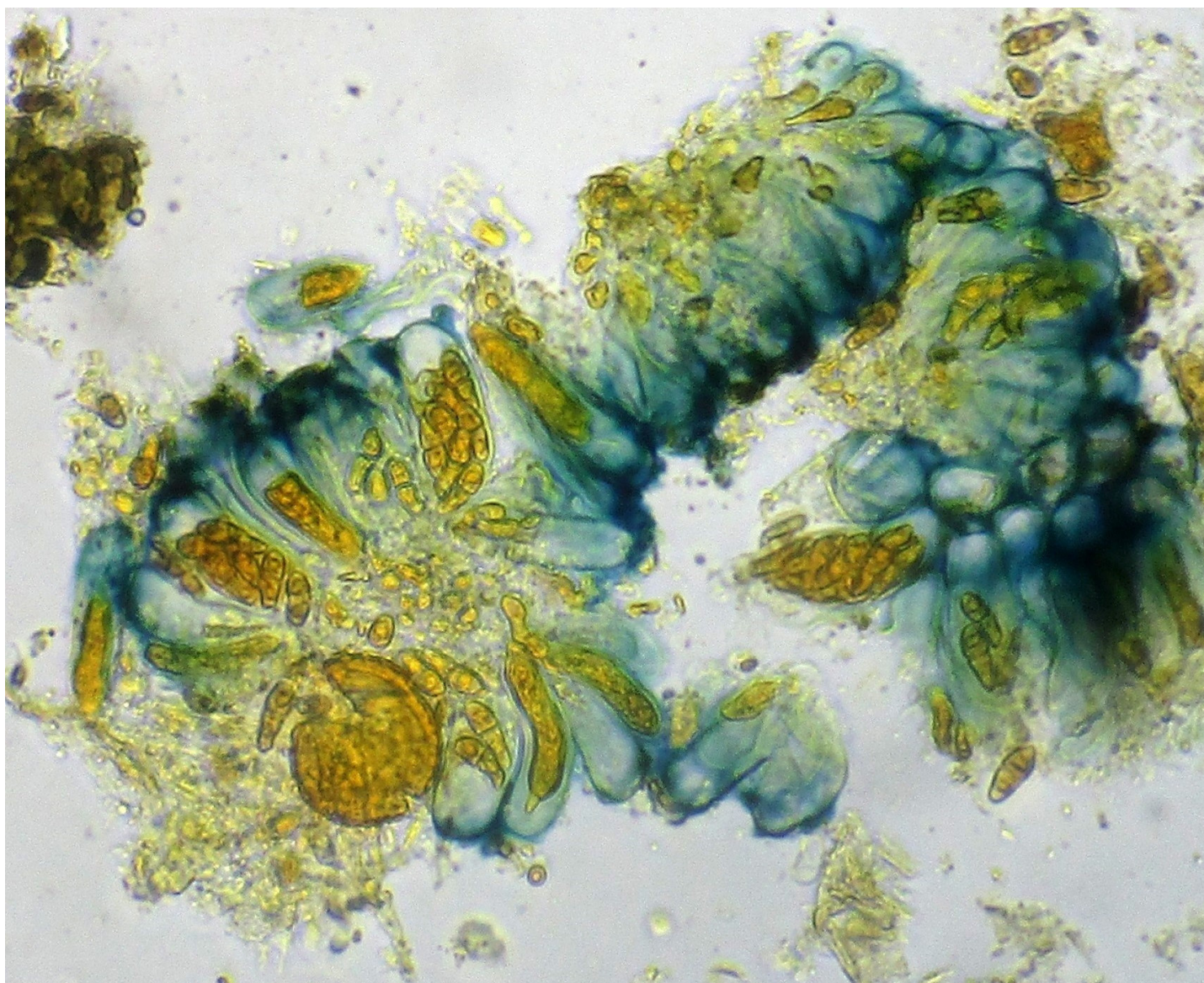
Ascomata composed of up to 1 mm elongate, isolated apotheci with a coriaceous consistency; peridium thin, glabrous, dark brown in colour; at maturity opening longitudinally like a slit and exposing a pale hymenial surface.

Ascospores 12.6–13.9 × 4.6–6.0 µm, on average 13.2 × 5.5 µm, Q = 2.28–2.68, on average 2.44; narrowly clavate with slightly restricted septum more or less in the median position; hyaline, light brown in Melzer's reagent.

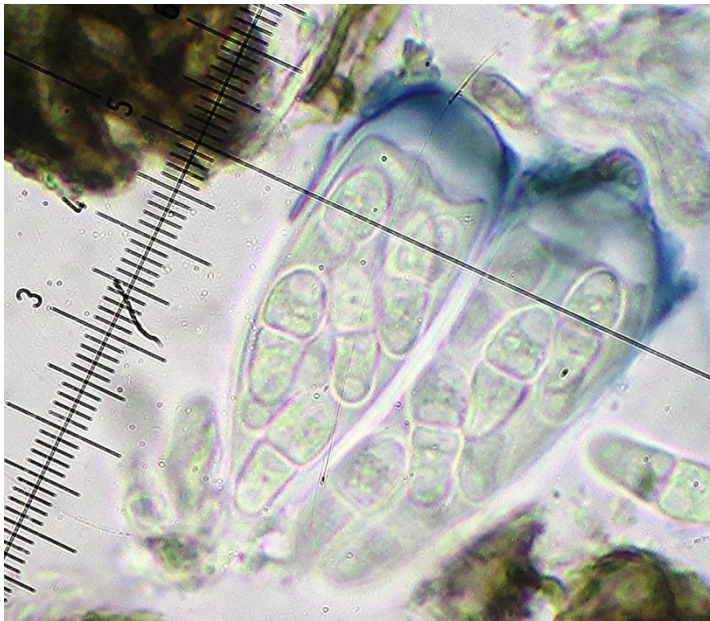
Asci 35.6–50.0 × 12.3–17.0 µm, mostly ellipsoid-clavate to narrowly clavate, mostly sessile, 8-spored, bitunicate, walls thickened at the apex; apex broadly rounded to subtruncate, turning blue with Melzer's reagent (amyloid).

Pseudoparaphyses not observed.

Collection examined and Habitat: Bosnia and Herzegovina, Prijedor; growing scattered, saprobic on wet soil on debarked branches of *Thuja* sp. abundantly covered with litter of two-year-old stems of decayed *Carex* sp., also plants of *Juncus* sp. nearby; 2 March 2025, legit D. Trivič (in pers. herb.).



Hymenium in Melzer's reagent



Asci in Melzer's reagent



Ascospores in Melzer's reagent

NOTES

Hysteropeltella moravica was first described in 1923 on ferns (*Aspidium filix-mas*, currently known as *Dryopteris filix-mas*) from central Europe, in the Czech region of Moravia. The only other heterotypic description known so far is that of Holm & Holm (1978) on ferns from Sweden which expands its diffusion to North Europe.

The Bosnian collection introduces its presence in the Balkans and its growth on a different substrate, apparently composed of debarked dead *Thuja sp.* branches but which are covered with abundant fragments of two-year-old decayed *Carex* stems, so that the possible presence of minuscule *Carex* particles cannot be ruled out. These data seem to confirm an ecological preference for plants that love moist to wet substrates.

The synoptic table below shows the dimensions of the spores and asci taken from the consulted literature.

Author	ascospores	asci
Petrak (1923), protolog	12–15 × 5–6.5 µm	32–44 × 12–15 µm (30 × 18–20 µm when ovoid)
Holm & Holm (1978), on ferns in Sweden	11–13 × 5 µm	30–36 × 12–15 µm
Ariyawansa <i>et al.</i> (2013), type revision	10–18 × 4–6 µm, av. 15 × 4 µm	35–45 × 15–25 µm, av. 40 × 20 µm

Holm & Holm (1978) and Ariyawansa *et al.* (2013) report that mature ascospores acquire a light brown pigmentation.

REFERENCES

- Ariyawansa, HA; Kang, JC; Alias, SA; Chukeatirote; Hyde, KD (2013) Towards a natural classification of *Dothideomycetes*: the genera *Dermatodothella*, *Dothideopsella*, *Grandigallia*, *Hysteropeltella* and *Gloeodiscus* (*Dothideomycetes incertae sedis*). *Phytotaxa* **147**:35–47
<http://dx.doi.org/10.11646/phytotaxa.147.2.1>
- Holm, L; Holm, K (1978) Some pteridicolous *Ascomycetes*. *Bot. Notiser* **131**:97–115
- Lumbsch, HT; Huhndorf, SM (2010) Outline of *Ascomycota* – 2009. *Fieldiana Life and Earth Sciences* **1**:1–60
- Petrak, F (1923) Mykologische Notizen. V. *Annales Mycologici* **21**(1–2):1–69
- Yacharoen, S; Tian, Q; Chomnunti, P; Boonmee, S; Chukeatirote, E; Bhat, JD; Hyde, KD (2015) *Patellariaceae* revisited. *Mycosphere* **6**(3):290–326
<https://doi.org/10.5943/mycosphere/6/3/7>